

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:04:54 ; Search time 25.404 Seconds
(without alignments)
1503.623 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSRPPLMLLLVLS.....PRLPILSILPLILLQTLW 397
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	2 JE0082	GPI-linked recepto
2	132	6.2	4544	1 S02392	alpha-2-macroglobu
3	131	6.1	4545	1 S25111	alpha-2-macroglobu
4	124	5.8	1722	2 E89753	protein Filic7.4 [1
5	123	5.8	1964	2 T09059	notch4 - mouse
6	120.5	5.7	2531	2 A46019	notch-1 protein -
7	118	5.5	2555	2 A40043	notch protein homo
8	117	5.5	1746	1 S19694	tenascin precursor
9	117	5.5	4543	1 A53102	alpha-2-macroglobu
10	114.5	5.4	2531	2 S18188	notch protein homo
11	114	5.3	2437	2 S42612	transmembrane prot
12	112.5	5.3	2703	1 A24420	notch protein - fr
13	110	5.2	965	2 S62935	hypothetical prote
14	110	5.2	1187	2 T18355	hypothetical prote
15	110	5.2	2321	2 S78549	notch3 protein - h
16	109.5	5.1	2233	2 T28669	surface protein 51
17	109	5.1	1047	2 D71302	probable exonuclea
18	108	5.1	1394	2 A35626	transforming growt
19	108	5.1	1712	2 A38261	masking protein pr
20	108	5.1	1847	2 T18308	probable vitellog
21	107.5	5.0	996	2 JE0237	apolipoprotein E r
22	107.5	5.0	2150	2 T32497	hypothetical prote
23	107	5.0	3051	2 S42373	hypothetical prote
24	106.5	5.0	2019	1 JQ1322	tenascin precursor
25	106	5.0	2918	2 A54105	fibillin-2 precur
26	105.5	5.0	384	2 S25771	gas1 protein - mou
27	105.5	5.0	873	1 A49729	VLDL receptor prec
28	105	4.9	1077	2 T41146	probable cysteine-
29	105	4.9	1106	2 T13938	gene shuttle craft

30	105	4.9	1408	2 S16148	gene serrate prote
31	104.5	4.9	1203	2 A49175	Notch B protein -
32	103.5	4.9	869	1 JC4858	VLDL receptor prec
33	103	4.8	886	2 A57172	probable hormone r
34	103	4.8	2318	2 S45306	notch 3 protein -
35	102.5	4.8	835	2 JP0076	nel protein - chic
36	102.5	4.8	1188	2 D86236	protein Fl4N23.5 [
37	102	4.8	1220	2 A56136	jagged protein pre
38	101.5	4.8	593	1 GYHU	granulin precursor
39	100.5	4.7	5376	2 T42215	zonadhesin - mouse
40	100	4.7	728	2 T50719	C-Delta-1 - chicke
41	100	4.7	1106	2 T44598	hypothetical prote
42	99.5	4.7	2471	2 A49128	cell-fate determin
43	99.5	4.7	2718	2 A23475	G surface protein
44	99	4.6	2704	2 S09118	G surface protein
45	99	4.6	2907	2 A57278	fibillin-2 precur

ALIGNMENTS

RESULT 1

JE0082
GPI-linked receptor precursor - mouse
N;Alternate names: GFRalpha-3
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JE0082
R;Nomenclature: S.; Ito, S.; Yang, L.X.; Kiuchi, K.
Biochem. Biophys. Res. Commun. 244, 849-853, 1998
A;Title: Molecular cloning and expression analysis of GFRalpha-3, a novel cDNA related t
A;Reference number: JE0082; MUID:98205811; PMID:9535755
A;Accession: JE0082
A;Molecule type: mRNA
A;Residues: 1-397 <NOM>
A;Cross-references: UNIPROT:O35118; UNIPARC:UPI0000002231A; DBJ:AB088833; NID:92627159;
C;Comment: This protein plays a distinct role in cell survival and differentiation.
C;Superfamily: Mus musculus GPI-linked receptor
C;Keywords: glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;380-397/Region: hydrophobic
F;92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%;	Score 2131;	DB 2;	Length 397;
Best Local Similarity	100.0%;	Pred. No. 8.2e-166;		
Matches	397;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	MGLSWSRPPLMLLLVLSILWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH	60	
Db	1	MGLSWSRPPLMLLLVLSILWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH	60	
Qy	61	LGSTCTSLSRPLPLEESAMSDCLAEAEQLRNSLIDCRCHRRMKHOATCLDIYTVTHPA	120	
Db	61	LGSTCTSLSRPLPLEESAMSDCLAEAEQLRNSLIDCRCHRRMKHOATCLDIYTVTHPA	120	
Qy	121	RLSGDYELDVSPYEDVTTSKPKWNLSKLNKLKPDSDCLCKFAMLCCTLHKDCDLRKAYG	180	
Db	121	RLSGDYELDVSPYEDVTTSKPKWNLSKLNKLKPDSDCLCKFAMLCCTLHKDCDLRKAYG	180	
Qy	181	EACSGIRCOHCLIAQLRSFFEKAAESHAOGLLLCPCAPEDAGGERRNTIAPSCALPS	240	
Db	181	EACSGIRCOHCLIAQLRSFFEKAAESHAOGLLLCPCAPEDAGGERRNTIAPSCALPS	240	
Qy	241	VTNCLDLRSFCRADPLCRSLMDPOTHCHPMDILGTFCATEQSRCLRAYLGLIGTAMTPN	300	
Db	241	VTNCLDLRSFCRADPLCRSLMDPOTHCHPMDILGTFCATEQSRCLRAYLGLIGTAMTPN	300	
Qy	301	FISKVNTVALSCTCRSGNQLQDECEQLERSFSPNCLVEAIAAKMFHRLQFSQDWADS	360	
Db	301	FISKVNTVALSCTCRSGNQLQDECEQLERSFSPNCLVEAIAAKMFHRLQFSQDWADS	360	
Qy	361	TFSVVQOQNSNPALRQPLPILSILPILLQTLW	397	

Db 361 TFSVVQQNSNPALRQLPRLPIILSFILPLLILQTLN 397

RESULT 2

alpha-2-macroglobulin receptor precursor - human

N/Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor

C/Species: Homo sapiens (man)

C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C/Accession: S02392; S30027; I37998; S49210; S12538

R/Herz, J.; Hamann, U.; Rogne, S.; Myklebost, O.; Gausepohl, H.; Stanley, K.K.

EMBO J. 7, 4119-4127, 1988

A/Title: Surface location and high affinity for calcium of a 500-kd liver membrane protein

A/Reference number: S02392; MUID:89210795; PMID:3266596

A/Accession: S02392

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-4544 <HER>

A/Cross-references: UNIPROT:Q07954; UNIPARC:UPI0000055B03; EMBL:X13916; NID:g34338; PIDN:R1312598; T. Kristensen, T.

A/Reference number: S30027

A/Accession: S30027

A/Molecule type: mRNA

A/Residues: 3275-3864 <KRI>

A/Cross-references: UNIPARC:UPI00001736CD; EMBL:X55077

R/Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.

EMBO J. 9, 1769-1776, 1990

A/Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related protein

A/Reference number: S12538; MUID:90269210; PMID:2112085

A/Contents: annotation: site of proteolytic cleavage

R/Kutt, H.; Herz, J.; Stanley, K.K.

Biochem. Biophys. Acta 1009, 229-236, 1989

A/Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promotes

A/Reference number: I37998; MUID:90089395; PMID:2597675

A/Accession: I37998

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-11 <RES>

A/Cross-references: UNIPARC:UPI0000000A1E; EMBL:X15424; NID:g34408; PIDN:CAA33464.1; PID:R1312598; J. Biol. Chem. 265, 17401-17404, 1990

A/Title: Sequence identity between the alpha2-macroglobulin receptor and low density lip

A/Reference number: A39210; MUID:91009181; PMID:1698775

A/Accession: A39210

A/Status: preliminary

A/Molecule type: protein

A/Residues: 150-166;234-238,'X',240-245,'X',247-252,'G',686-695;902-916;1096-1109;'S',17

A/Cross-references: UNIPARC:UPI00001736CB; UNIPARC:UPI00001736CF; UNIPARC:UPI00001736D0; GDS; UNIPARC:UPI00001736D6; UNIPARC:UPI00001736D7

C/Genetics:

A/Gene: GDB:LRP1; APR; LRP; A2MR

A/Cross-references: GDB:119694; OMIM:107770

A/Map position: 12q13.1-12q13.3

C/Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated proteins

C/Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <S15K>

F/27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F/72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F/115-148/Domain: EGF homology <EG1>

F/154-188/Domain: EGF homology <EG2>

F/198-239/Domain: LDL receptor WYTD-containing repeat homology <YW01>

F/240-281/Domain: LDL receptor WYTD-containing repeat homology <YW02>

F/292-334/Domain: LDL receptor WYTD-containing repeat homology <YW03>

F/335-378/Domain: LDL receptor WYTD-containing repeat homology <YW04>

F/379-420/Domain: LDL receptor WYTD-containing repeat homology <YW05>

F/421-468/Domain: LDL receptor WYTD-containing repeat homology <YW06>

F/478-519/Domain: EGF homology <EG3>

F/571-613/Domain: LDL receptor WYTD-containing repeat homology <YW07>

F/614-659/Domain: LDL receptor WYTD-containing repeat homology <YW08>

F/660-710/Domain: LDL receptor WYTD-containing repeat homology <YW09>

F/711-752/Domain: LDL receptor WYTD-containing repeat homology <YW10>

F/753-799/Domain: LDL receptor WYTD-containing repeat homology <YW11>

F/807-842/Domain: EGF homology <EG4>

F/854-890/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F/895-931/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F/936-971/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F/976-1011/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F/1015-1051/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F/1062-1097/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F/1104-1140/Domain: LDL receptor ligand-binding repeat homology <LDL9>

F/1145-1182/Domain: LDL receptor ligand-binding repeat homology <LDL10>

F/1185-1221/Domain: EGF homology <EG5>

F/1227-1261/Domain: EGF homology <EG6>

F/1269-1308/Domain: LDL receptor WYTD-containing repeat homology <YW12>

F/1309-1355/Domain: LDL receptor WYTD-containing repeat homology <YW13>

F/1356-1398/Domain: LDL receptor WYTD-containing repeat homology <YW14>

F/1399-1445/Domain: LDL receptor WYTD-containing repeat homology <YW15>

F/1446-1488/Domain: LDL receptor WYTD-containing repeat homology <YW16>

F/1489-1531/Domain: LDL receptor WYTD-containing repeat homology <YW17>

F/1540-1578/Domain: EGF homology <EG7>

F/1583-1626/Domain: LDL receptor WYTD-containing repeat homology <YW18>

F/1627-1669/Domain: LDL receptor WYTD-containing repeat homology <YW19>

F/1670-1713/Domain: LDL receptor WYTD-containing repeat homology <YW20>

F/1714-1753/Domain: LDL receptor WYTD-containing repeat homology <YW21>

F/1754-1796/Domain: LDL receptor WYTD-containing repeat homology <YW22>

F/1797-1846/Domain: LDL receptor WYTD-containing repeat homology <YW23>

F/1850-1886/Domain: EGF homology <EG8>

F/1934-1976/Domain: LDL receptor WYTD-containing repeat homology <YW24>

F/1977-2019/Domain: LDL receptor WYTD-containing repeat homology <YW25>

F/2020-2063/Domain: LDL receptor WYTD-containing repeat homology <YW26>

F/2064-2105/Domain: LDL receptor WYTD-containing repeat homology <YW27>

F/2106-2151/Domain: LDL receptor WYTD-containing repeat homology <YW28>

F/2159-2194/Domain: EGF homology <EG9>

F/2199-2241/Domain: LDL receptor WYTD-containing repeat homology <YW29>

F/2253-2294/Domain: LDL receptor WYTD-containing repeat homology <YW30>

F/2344-2388/Domain: LDL receptor WYTD-containing repeat homology <YW31>

F/2389-2429/Domain: LDL receptor WYTD-containing repeat homology <YW32>

F/2430-2473/Domain: LDL receptor WYTD-containing repeat homology <YW33>

F/2482-2517/Domain: EGF homology <EG10>

F/2524-2561/Domain: LDL receptor ligand-binding repeat homology <LDLB>

F/2566-2600/Domain: LDL receptor ligand-binding repeat homology <LDLC>

F/2605-2639/Domain: LDL receptor ligand-binding repeat homology <LDLD>

F/2652-2688/Domain: LDL receptor ligand-binding repeat homology <LDLE>

F/2696-2730/Domain: LDL receptor ligand-binding repeat homology <LDLF>

F/2734-2769/Domain: LDL receptor ligand-binding repeat homology <LDLG>

F/2774-2812/Domain: LDL receptor ligand-binding repeat homology <LDLH>

F/2818-2853/Domain: LDL receptor ligand-binding repeat homology <LDLI>

F/2858-2897/Domain: LDL receptor ligand-binding repeat homology <LDLJ>

F/2904-2939/Domain: LDL receptor ligand-binding repeat homology <LDLK>

F/2944-2980/Domain: EGF homology <EG11>

F/2986-3021/Domain: EGF homology <EG12>

F/3029-3068/Domain: LDL receptor WYTD-containing repeat homology <YW34>

F/3069-3113/Domain: LDL receptor WYTD-containing repeat homology <YW35>

F/3114-3156/Domain: LDL receptor WYTD-containing repeat homology <YW36>

F/3157-3200/Domain: LDL receptor WYTD-containing repeat homology <YW37>

F/3201-3241/Domain: LDL receptor WYTD-containing repeat homology <YW38>

F/3242-3284/Domain: LDL receptor WYTD-containing repeat homology <YW39>

F/3294-3330/Domain: EGF homology <EG13>

F/3334-3369/Domain: LDL receptor ligand-binding repeat homology <LDLM>

F/3374-3408/Domain: LDL receptor ligand-binding repeat homology <LDLN>

F/3413-3448/Domain: LDL receptor ligand-binding repeat homology <LDLO>

F/3453-3489/Domain: LDL receptor ligand-binding repeat homology <LDLP>

F/3494-3531/Domain: LDL receptor ligand-binding repeat homology <LDLQ>

F/3536-3570/Domain: LDL receptor ligand-binding repeat homology <LDLR>

F/3575-3609/Domain: LDL receptor ligand-binding repeat homology <LDLS>

F/3613-3647/Domain: LDL receptor ligand-binding repeat homology <LDLT>

F/3654-3690/Domain: LDL receptor ligand-binding repeat homology <LDLU>

F/3695-3731/Domain: LDL receptor ligand-binding repeat homology <LDLV>

F/3741-3776/Domain: LDL receptor ligand-binding repeat homology <LDLW>

F/3785-3822/Domain: EGF homology <EG14>

F/3828-3860/Domain: EGF homology <EG15>

F/3868-3911/Domain: LDL receptor WYTD-containing repeat homology <YW40>

F:2945-2981/Domain: EGF homology <EG11>
F:2987-3022/Domain: EGF homology <EG12>
F:3030-3069/Domain: LDL receptor WYTD-containing repeat homology <YW34>
F:3070-3114/Domain: LDL receptor WYTD-containing repeat homology <YW35>
F:3115-3157/Domain: LDL receptor WYTD-containing repeat homology <YW36>
F:3158-3201/Domain: LDL receptor WYTD-containing repeat homology <YW37>
F:3202-3242/Domain: LDL receptor WYTD-containing repeat homology <YW38>
F:3243-3285/Domain: LDL receptor WYTD-containing repeat homology <YW39>
F:3295-3331/Domain: EGF homology <EG13>
F:3335-3370/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F:3375-3409/Domain: LDL receptor ligand-binding repeat homology <LDLM>
F:3414-3449/Domain: LDL receptor ligand-binding repeat homology <LDLN>
F:3454-3490/Domain: LDL receptor ligand-binding repeat homology <LDLO>
F:3495-3532/Domain: LDL receptor ligand-binding repeat homology <LDLP>
F:3537-3571/Domain: LDL receptor ligand-binding repeat homology <LDLQ>
F:3576-3610/Domain: LDL receptor ligand-binding repeat homology <LDLR>
F:3614-3648/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F:3655-3691/Domain: LDL receptor ligand-binding repeat homology <LDLT>
F:3696-3732/Domain: LDL receptor ligand-binding repeat homology <LDLU>
F:3743-3777/Domain: LDL receptor ligand-binding repeat homology <LDLV>
F:3786-3823/Domain: EGF homology <EG14>
F:3829-3861/Domain: EGF homology <EG15>
F:3869-3912/Domain: LDL receptor WYTD-containing repeat homology <YW40>
F:3913-3970/Domain: LDL receptor WYTD-containing repeat homology <YW41>
F:3945-4545/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
F:3945-4421/Domain: 85K chain extracellular #status predicted <EXT>
F:3971-4013/Domain: LDL receptor WYTD-containing repeat homology <YW42>
F:4014-4057/Domain: LDL receptor WYTD-containing repeat homology <YW43>
F:4058-4100/Domain: LDL receptor WYTD-containing repeat homology <YW44>
F:4101-4143/Domain: LDL receptor WYTD-containing repeat homology <YW45>
F:4152-4183/Domain: EGF homology <EG16>
F:4201-4232/Domain: EGF homology <EG17>
F:4237-4268/Domain: EGF homology <EG18>
F:4273-4304/Domain: EGF homology <EG19>
F:4309-4340/Domain: EGF homology <EG20>
F:4345-4375/Domain: EGF homology <EG21>
F:4378-4409/Domain: EGF homology <EG22>
F:4422-4445/Domain: transmembrane #status predicted <TMM>
F:4446-4545/Domain: intracellular #status predicted <INT>
F:167,2993/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:2959/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:4076,4156,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 131; DB 1; Length 4545;
Best Local Similarity 19.8%; Pred. No. 0.052;
Matches 78; Conservative 39; Mismatches 131; Indels 146; Gaps 21;

QY 62 GSCTSLSRPLPLEESAMGADCLAEAEQLRNSSLIDCRCHRM-----KHOATCL 111
DB 2616 GSCIGNSSR-----CNQFVDCEDADEM-NCSATDCSSVFRIGVGVLFPQCERTSLCY 2668

QY 112 DIYVTHVPARSLGDYELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLKFAMLCITLHDK 171
DB 2669 APSWVDCGANDCGD-----YSDERDCPGVKPRCPFLNYFACPSGRCIPMSWTCDKEDD 2721

QY 172 CDRLRKAYGE-----ACS-GIRQPHLCIAQ-----LRSFPEKAESHAQG-- 211
DB 2722 CEN-----GEDETHCNKFCSEAQFEQNHRCISKQWLCDGSDDCGDSDEAA--HCEGKT 2774

QY 212 ----LLICP-----CAPE-----DAGCGERR----RNTI----- 232
DB 2775 CGPSSFCPTGTHCVPERWLCDGDKDCTDGADSVTAGCLYNSTCDDREPMQNRLCIPK 2834

QY 233 -----APSCALPSVTPN-----CLDRSF-CRADPLCRSLRMDFTQ 267
DB 2835 HFVCDHRRDCADGSDSPECEYPTCGNEFRFCANGRCSSRQWCECGDNDCHDHSDEAPK 2894

QY 268 HCHPMDILGTCATEQSRCLRAYLGLTGATMTPNFIKVVNTTVALSCTCRSGNLDQEC-- 325
DB 2895 NPH-----CTSPENHC-----NASSQFLCSSGRCVBAALLCNG-----QDDCGD 2933

QY 326 EQLERSFSQNPCLVEAIAAKMRFRHQLFSQDWAD 359

Db 2934 GSDRGCHVNECLSRKLSG-----CSQDCED 2959

RESULT 4
E89753
protein F11C7.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89753
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A:Accession: E89753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1722 <STO>
A:Cross-references: UNIPROT:Q19350; UNIPARC:UPI0000074975; GB:chr_X; PIDN:AAC69012.1; P
C:Genetics:
A:Gene: F11C7.4
A:Map position: X

Query Match 5.8%; Score 124; DB 2; Length 1722;
Best Local Similarity 19.9%; Pred. No. 0.071;
Matches 75; Conservative 53; Mismatches 156; Indels 92; Gaps 21;

QY 34 ENRFVNSTQ---ARKKC---BANPACKAAYOHLGS-CTSSLSRPLPLEESAMSDCLEA 86
DB 1327 EQRDVNECNHYDCNRGHCVMTVSGPACQCEMGYTGRCFCKLJN-----QCSNNTCSSRGA 1381

QY 87 AQLRNSSLIDC-----RCHRMKHQATCLDIYVTHVPARSLGDYELDVSPYEDTVTS 139
DB 1382 CSPVWNNTVCNDDNNWRGAHQHMD---TCLDF-----PCWNDG----- 1418

QY 140 KPWKNLSKLNMLKPDSDLCLKFAM--LCTLHDKDLRKAYGEACSGIRCORHLCLAQ 197
DB 1419 -----VCTNDENTFSCQKFFPMGTRCEISGSLKACQVHGE-CIQLSPETHTSCNI 1471

QY 198 RSFFKAESHAQGLLLPCAPEDAGCGRRRNTTAPSALPSVTPNC---LD--LRSPC 252
DB 1472 -GYEGDADCCKIDYCKAGPCL-NGANC-ENKLTGYKCTCAVGFEAGADCEINIDECALFEC 1528

QY 253 RADPLCRSLMDPQTHCHPMDILG-TCATEQSRCLRAYLGLTGATMTPNFIK--VNTTV 309
DB 1529 KNGAKCRDKINDYECVCDGTGFEGRNCTTDINEC-----ANPNINCINGECTNTLG 1578

QY 310 ALSCTCRSGNLDQECQELERSFSQNPCLVEAIAAKMRFRHQLFSQDWADSTFSVVOQQN 369
DB 1579 NYKACR-NGFIGPRCS-----VRNPCTAQIASNNI-----SSVTCVHGKC 1618

QY 370 SNPALRLQPLPILSF 385
DB 1619 VNPVQVQIEKNREVAKY 1634

RESULT 5
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S.
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:G2564945;
C:Genetics:

Db	652	SGTCLDKIDGYEACPEPGYTGSMCNVNIDECAGSPCHNGTGEDGIAGFTCKCPGY----	708
Qy	293	IGTAMTPNFIKVNITVALSC---TCRGSNG-----LQDECEQLRSF	332
Db	709	----HDPTCLSEVNECNSNPCIHGACRDGLNGYKDCAPGWSGTNCDINNNECE-----	758
Qy	333	SONPCL	338
Db	759	-SNPCV	763
RESULT 7			
A40043			
notch protein homolog TAN-1 precursor - human			
C:Species: Homo sapiens (man)			
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 05-Oct-2004			
C:Accession: A40043			
R:Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-661, 1991			
A:Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal			
A:Reference number: A40043; MUID:91347367; PMID:1831692			
A:Accession: A40043			
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra			
A:Molecule type: mRNA			
A:Residues: 1-2555 <ELL>			
A:Cross-references: UNIPARC:UPI0000177455; GB:M73980			
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology			
F:261-292/Domain: EGF homology <EGX1>			
F:494-525/Domain: EGF homology <EGF1>			
F:987-1018/Domain: EGF homology <EGX2>			
F:1149-1180/Domain: EGF homology <EGF>			
F:1187-1218/Domain: EGF homology <EGF3>			
F:1233-1264/Domain: EGF homology <EGX3>			
F:1927-1959/Domain: ankyrin repeat homology <AN1>			
F:1960-1992/Domain: ankyrin repeat homology <AN2>			
F:1994-2026/Domain: ankyrin repeat homology <AN3>			
F:2027-2059/Domain: ankyrin repeat homology <AN4>			
F:2060-2092/Domain: ankyrin repeat homology <AN5>			
Query Match 5.5%; Score 118; DB 2; Length 2555;			
Best Local Similarity 20.4%; Pred. No. 0.33;			
Matches 85; Conservative 46; Mismatches 136; Indels 150; Gaps 26;			
Qy	39	NSTQARKKEANPACKAAAYQHLGSGCTSSLSRPL-----PLEESAMSD-CLEAAEQLRNRS	94
Db	379	NPCNEG-SNCDTNPVNGKA---ICTCPSGYTGPAQSQDVDECSLGANPCEHAGKINTLIG	434
Qy	95	LIDCRC-----HRRMKHOATCLDIYWTVHPARSLGVDYELVSP-YE--	134
Db	435	SPECQCLQGYTGPRCEIDVNECVSNPCQNDATCLD-----QIGEFQCMFQYEGV	485
Qy	135	-----DTVTSKPWKN-----LSKLN-----MLKPSDCLCK-----	161
Db	486	HCEWNTDECASSFLANGRCCLDKINEFQCEPCTGFTGHLQDVDECASTPCKNGAKCLDG	545
Qy	162	----FAMLC-----LH-----DKCDRLRKAYGACSGIRQORHLCLAQLRSPFEKAAESH	208
Db	546	PNTYTCVCTEGYTGTHCEVDIDCEDPDPCHYGCKDGVATFTCLCRP-----GYTGHHCETN	602
Qy	209	AQGLLLCPCA-----PEDAGGERRRNTIAPSCAL-----PSVTPNCILD-LRSF-	251
Db	603	INECSSQPCNLRTQCDPDNAYLCFLKGTGTGNCEINLDDCASSPCDSGTCLDKIDGYE	662
Qy	252	CRADP-----LCRSRLMDFQTH-CHPMDILGTCATE-----QSRCLRAYLGLIGTAMTPNF	301
Db	663	CACEPGYTGSMCNINDECAGNPCNG---GTCTEDGINGFTCRCPGY-----HDPTC	712
Qy	302	ISKVNITVALSC---TCRGSNG-----LQDECEQLRSFSQNPL	338
Db	713	LSEVNECNSNPCVHAGACRDSLNGYKDCDPPGWSGTNCDINNNECE-----SNPCV	762

RESULT 8			
S19694			
tenascin precursor - pig			
N:Alternate names: contactin; hexabrachion			
C:Species: Sus scrofa domestica (domestic pig)			
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C:Accession: S19694			
R:Niehi, T.; Weinstein, J.; Gillespie, W.M.; Paulson, J.C.			
Eur. J. Biochem. 202, 643-648, 1991			
A:Title: Complete primary structure of porcine tenascin. Detection of tenascin transcrip			
A:Reference number: S19694; MUID:92104189; PMID:1722152			
A:Accession: S19694			
A:Molecule type: mRNA			
A:Residues: 1-1746 <NIS>			
A:Cross-references: UNIPROT:Q29116; UNIPARC:UPI0000136BBB; EMBL:X61599; NID:g2124; PIDN			
C:Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type			
C:Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracel			
F:1-22/Domain: signal sequence #status predicted <SIG>			
F:23-1746/Product: tenascin #status predicted <MAT>			
F:346-372/Domain: EGF homology <EGF>			
F:377-403/Domain: EGF homology <EGF2>			
F:622-703/Domain: fibronectin type III repeat homology <FN3A>			
F:711-793/Domain: fibronectin type III repeat homology <FN3B>			
F:802-884/Domain: fibronectin type III repeat homology <FN3C>			
F:892-976/Domain: fibronectin type III repeat homology <FN3D>			
F:984-1064/Domain: fibronectin type III repeat homology <FN3E>			
F:1073-1155/Domain: fibronectin type III repeat homology <FN3F>			
F:1164-1246/Domain: fibronectin type III repeat homology <FN3G>			
F:1254-1335/Domain: fibronectin type III repeat homology <FN3H>			
F:1343-1423/Domain: fibronectin type III repeat homology <FN3I>			
F:1431-1511/Domain: fibronectin type III repeat homology <FN3J>			
F:1526-1734/Domain: fibronectin type III repeat homology <FBG>			
F:38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (Asn) (covalent) #s			
Query Match 5.5%; Score 117; DB 1; Length 1746;			
Best Local Similarity 21.5%; Pred. No. 0.27;			
Matches 90; Conservative 33; Mismatches 150; Indels 146; Gaps 22;			
Qy	43	QARKKEANPACKAAAYQHLGSGCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHR	102
Db	351	RGRGRCEE-----GQCV-----CDEGFAGADCSE	379
Qy	103	RMKHOATCLDIYWTVHPARSLGVDYELVSPYEDTVTSPKMNLSKLNMLKPSDLCL--L	160
Db	380	DCHNRGRCLD-----GRCECD-DGPE-----GEDCGEL	406
Qy	161	KFAMLCITLHDK-----CDRLRKAYGACSGIRQ-----RHLCLAQLRSPFEKAAESH	208
Db	407	RCFGGCSGHRGCVNGQCVCDGRT--GEDCSQLRCPNDCHGRGCV-QGRCEHGFGQY	463
Qy	209	AQGLLLCP-----CAPEDAGGERRRNTIAPS-----CALPSV	241
Db	464	DCSEMSCPHDCHQHRGCVNGCMVCDGDTGDECRELRCPGDCSQRCQVDCRCVCEHGA	523
Qy	242	TPNCLDLRSFCRADPLCRSRLMDFQTHC-----PMDI--LGTCAEQSRCL	286
Db	524	GFDCADLA--CFSDCHGRGCVNGQCVCHGFTGDKGQRRCPGDCGQRCVVGQCVCH	581
Qy	287	RAYLGL-IGTAMTPNFIKVNITVALSCTCRSGNMLQDECEQLRSFSQNPLVEIAIA--	344
Db	582	EGFTGLDCCQRSQPCNDCSNWGQCVSGRCIC-NEGYSGEDCSQVS---PPKDLIVTVEE	637
Qy	345	-----KMRFHROLF-----SQWADSTFVQQNSNPALRQLRPLP--ILSFSIL	388
Db	638	TYNLAWDNEMRWTEYLIVYTPHTHEDGLEMQFRVPGDTSTTIRELEPGVEYFIRVAIL	696

RESULT 9			
A53102			
alpha-2-macroglobulin receptor precursor - chicken			
N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein recept			
C:Species: Gallus gallus (chicken)			
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004			

C;Accession: A53102

R;Nimpt, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.

J. Biol. Chem. 269, 212-219, 1994

A;Title: The somatic cell-specific low density lipoprotein receptor-related protein of b

A;Reference number: A53102; MUID:94103212; PMID:7506255

A;Accession: A53102

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-4543 <NIM>

A;Cross-references: UNIPROT:P98157; UNIPARC:UPI000013C4B3; GB:X74904; NID:G438006; PIDN:

C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated

d protein.

C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-3942/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>

F;18-3942, 3943-4543/Domain: alpha-2-macroglobulin receptor #status predicted <WAT>

F;29-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F;74-110/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F;117-150/Domain: EGF homology <EG1>

F;156-190/Domain: EGF homology <EG2>

F;200-241/Domain: LDL receptor WYTD-containing repeat homology <YW01>

F;242-283/Domain: LDL receptor WYTD-containing repeat homology <YW02>

F;294-336/Domain: LDL receptor WYTD-containing repeat homology <YW03>

F;337-380/Domain: LDL receptor WYTD-containing repeat homology <YW04>

F;381-422/Domain: LDL receptor WYTD-containing repeat homology <YW05>

F;423-470/Domain: LDL receptor WYTD-containing repeat homology <YW06>

F;480-521/Domain: EGF homology <EG3>

F;573-615/Domain: LDL receptor WYTD-containing repeat homology <YW07>

F;616-661/Domain: LDL receptor WYTD-containing repeat homology <YW08>

F;662-712/Domain: LDL receptor WYTD-containing repeat homology <YW09>

F;713-754/Domain: LDL receptor WYTD-containing repeat homology <YW10>

F;755-797/Domain: LDL receptor WYTD-containing repeat homology <YW11>

F;805-840/Domain: EGF homology <EG4>

F;852-888/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F;893-929/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F;934-969/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F;974-1009/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F;1013-1049/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F;1060-1095/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F;1102-1138/Domain: LDL receptor ligand-binding repeat homology <LDL9>

F;1143-1180/Domain: LDL receptor ligand-binding repeat homology <LDL10>

F;1188-1219/Domain: EGF homology <EG5>

F;1223-1259/Domain: EGF homology <EG6>

F;1267-1306/Domain: LDL receptor WYTD-containing repeat homology <YW12>

F;1307-1353/Domain: LDL receptor WYTD-containing repeat homology <YW13>

F;1354-1396/Domain: LDL receptor WYTD-containing repeat homology <YW14>

F;1397-1443/Domain: LDL receptor WYTD-containing repeat homology <YW15>

F;1444-1486/Domain: LDL receptor WYTD-containing repeat homology <YW16>

F;1487-1529/Domain: LDL receptor WYTD-containing repeat homology <YW17>

F;1538-1576/Domain: EGF homology <EG7>

F;1581-1624/Domain: LDL receptor WYTD-containing repeat homology <YW18>

F;1625-1667/Domain: LDL receptor WYTD-containing repeat homology <YW19>

F;1668-1711/Domain: LDL receptor WYTD-containing repeat homology <YW20>

F;1712-1751/Domain: LDL receptor WYTD-containing repeat homology <YW21>

F;1752-1794/Domain: LDL receptor WYTD-containing repeat homology <YW22>

F;1795-1842/Domain: LDL receptor WYTD-containing repeat homology <YW23>

F;1846-1882/Domain: EGF homology <EG8>

F;1930-1972/Domain: LDL receptor WYTD-containing repeat homology <YW24>

F;1973-2015/Domain: LDL receptor WYTD-containing repeat homology <YW25>

F;2016-2059/Domain: LDL receptor WYTD-containing repeat homology <YW26>

F;2060-2101/Domain: LDL receptor WYTD-containing repeat homology <YW27>

F;2102-2147/Domain: LDL receptor WYTD-containing repeat homology <YW28>

F;2155-2190/Domain: EGF homology <EG9>

F;2195-2237/Domain: LDL receptor WYTD-containing repeat homology <YW29>

F;2247-2288/Domain: LDL receptor WYTD-containing repeat homology <YW30>

F;2338-2382/Domain: LDL receptor WYTD-containing repeat homology <YW31>

F;2383-2423/Domain: LDL receptor WYTD-containing repeat homology <YW32>

F;2424-2467/Domain: LDL receptor WYTD-containing repeat homology <YW33>

F;2476-2511/Domain: EGF homology <EG10>

F;2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDLB>

F;2560-2594/Domain: LDL receptor ligand-binding repeat homology <LDLC>

F;2599-2633/Domain: LDL receptor ligand-binding repeat homology <LDLD>

F;2646-2682/Domain: LDL receptor ligand-binding repeat homology <LDLE>

F;2690-2724/Domain: LDL receptor ligand-binding repeat homology <LDLF>

F;2732-2767/Domain: LDL receptor ligand-binding repeat homology <LDLG>

F;2772-2810/Domain: LDL receptor ligand-binding repeat homology <LDLH>

F;2816-2851/Domain: LDL receptor ligand-binding repeat homology <LDLI>

F;2856-2895/Domain: LDL receptor ligand-binding repeat homology <LDLJ>

F;2902-2936/Domain: LDL receptor ligand-binding repeat homology <LDLK>

F;2941-2977/Domain: EGF homology <EG11>

F;2983-3018/Domain: EGF homology <EG12>

F;3026-3065/Domain: LDL receptor WYTD-containing repeat homology <YW34>

F;3066-3110/Domain: LDL receptor WYTD-containing repeat homology <YW35>

F;3111-3153/Domain: LDL receptor WYTD-containing repeat homology <YW36>

F;3154-3197/Domain: LDL receptor WYTD-containing repeat homology <YW37>

F;3198-3238/Domain: LDL receptor WYTD-containing repeat homology <YW38>

F;3239-3281/Domain: LDL receptor WYTD-containing repeat homology <YW39>

F;3291-3327/Domain: EGF homology <EG13>

F;3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDLL>

F;3371-3405/Domain: LDL receptor ligand-binding repeat homology <LDLM>

F;3410-3445/Domain: LDL receptor ligand-binding repeat homology <LDLN>

F;3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDLO>

F;3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDLP>

F;3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDLQ>

F;3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDLR>

F;3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDLS>

F;3651-3687/Domain: LDL receptor ligand-binding repeat homology <LDLT>

F;3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDLU>

F;3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDLV>

F;3783-3820/Domain: EGF homology <EG14>

F;3826-3858/Domain: EGF homology <EG15>

F;3866-3909/Domain: LDL receptor WYTD-containing repeat homology <YW40>

F;3910-3968/Domain: LDL receptor WYTD-containing repeat homology <YW41>

F;3943-4543/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>

F;3943-4420/Domain: 85K chain extracellular #status predicted <EXT>

F;3969-4011/Domain: LDL receptor WYTD-containing repeat homology <YW42>

F;4012-4055/Domain: LDL receptor WYTD-containing repeat homology <YW43>

F;4056-4098/Domain: LDL receptor WYTD-containing repeat homology <YW44>

F;4099-4141/Domain: LDL receptor WYTD-containing repeat homology <YW45>

F;4150-4181/Domain: EGF homology <EG16>

F;4199-4230/Domain: EGF homology <EG17>

F;4235-4266/Domain: EGF homology <EG18>

F;4271-4302/Domain: EGF homology <EG19>

F;4307-4338/Domain: EGF homology <EG20>

F;4343-4373/Domain: EGF homology <EG21>

F;4376-4408/Domain: EGF homology <EG22>

F;4421-4443/Domain: transmembrane #status predicted <TM>

F;4444-4543/Domain: intracellular #status predicted <INT>

F;116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643

3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) (covalent

F;168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F;2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 5.5%; Score 117; DB 1; Length 4543;

Best Local Similarity 20.3%; Pred. No. 0.72;

Matches 65; Conservative 33; Mismatches 134; Indels 88; Gaps 16;

QY 29 NSLATENRF-----VNSCTQARKKCANPACKAAYOHL-----GSCSTSLRPLPLESAMSA 81

Db 2569 NGRCVASRWCNGVDDGDSNDEVFCNKTSCTAETFCRDCGSCIGNSSR-----CNQFI 2622

QY 82 DCLAAARLQNSLLIDCRCH-----RMKHOATCLDIYTWVHPARSLGDVLDVS 131

Db 2623 DCDASDEM-NCTATDCSSYFKLVKGKTTFOKCENTSLCYAPSWCDGDCGD----- 2675

QY 132 PYEDVTTSKPMWNTSLKMLKPDSDLCLKFAMLTCLDKCDRLKAYCE-----ACS---- 184

Db 2676 -YSDBRNCFGGRKPKCPANYFACPGRCIPMTWTCKEDDCEN-----GEBTHCSERQD 2729

QY 185 -----GTRCQRHLCLAQLRSFFKAAE-----SHAQGLLCP-----CAP 219

Db 2730 KFCYVQECNHRICSLK--WVCGADDCGDSDESRCLTTCSTGSGFCQGVVCP 2787

QY 220 E-----DAGCGERRNTIAPSCALPSVTPNCLRLSPFRADPLC--RSRLMDFQTHC-- 269

Db 2788 ERWLCDGKDCADGADETLAAGC-----LYNNTCDEREPMCGNRQCIPKHFVCDHDDDCGD 2843

Qy 270 ----HPMDILGTFCATEQSRC 285
| | | | |
Db 2844 GSDESPECEYPTGCPHPFRFC 2863

RESULT 10

S18188
notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A:Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Cross-references: UNIPARC:UPI0000177456; EMBL:X57405; NID:G57634; PID:G57635
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:1987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF>
F:1233-1364/Domain: EGF homology <EGF2>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 5.4%; Score 114.5; DB 2; Length 2531;
Best Local Similarity 19.9%; Pred. No. 0.63;
Matches 85; Conservative 40; Mismatches 132; Indels 171; Gaps 26;

Qy 39 NSCTQARKKCEANPA-----CKAAYQHLGSCSSLSRPLPLEESAMSD-CLEAAEQLRN 92
| | | | |
Db 379 NFNCEG-SNCDTNPVNGKAICTCPRGYTPACSQ-----DVDECALGANPCEHAKCLNT 432
| | | | |
Qy 93 SSLIDCRC-----HRRMKHOATCLDIYWTVHPARSLGDYELDVSP-YE 134
| | | | |
Db 433 LGSFECQCLQYGTGPRCEIDVNECISNPCQNDATCLD-----QIGEFQCICMPGYE 483
| | | | |
Qy 135 -----DVTISKPKWKN-----LSKLN-----MLKPSDLCLK----- 161
| | | | |
Db 484 GYVCEINTDECASSPCLHNGRCVDKINEFLCQCPKFGSLHCQYDVDECASTPCKNAGKC 543
| | | | |
Qy 162 -----FAMLC-----LH-----DKDRLKAYGACSGIR-----CO-----RHLC LAQ 196
| | | | |
Db 544 LGQPNYTCVCTEGYGTGTHCEVDIDCDPDPHIGLCKDGVATFTCLCQPGYTGHCETN 603
| | | | |
Qy 197 LRSFFEKAESAQAQGLLLCFCAPEDAGCGERRNTIAPSCALPSPVTPNCLDLRSFCRADP 256
| | | | |
Db 604 IN-----ECHSQ-----PC--RHGGTCQDRDNYLCLCKGTTGFNCEINLLDCASN 649
| | | | |
Qy 257 ----LCRSRLMDPQTHCHP-----WDIL-----GTC-----ATEQSRCLRAYL 290
| | | | |
Db 650 CDGSGTCLDKIDGYECACEPGYTGSMCNVNIDECAGSPCHNGGTGTCEDGIAGFTCRCEGY- 708
| | | | |
Qy 291 GLIGTAMTNFISKVNTTVALSC---TCRSGN-----LQDECEQLER 330
| | | | |
Db 709 -----HDPCTCLSEVNECNSNPCIHGACRDLGNGYKCDCAPGWSGTNCDINNECE---- 758
| | | | |
Qy 331 SFSQNPCL 338
| | | | |
Db 759 ----SNECV 763
| | | | |

RESULT 11

S42612
transmembrane protein precursor - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 20-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004

C:Accession: S42612
R:Bierkamp, C.; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A:Title: A zebrafish homolog of the Drosophila neurogenic gene Notch and its pattern o
A:Reference number: S42612; MUID:94128602; PMID:8297791
A:Accession: S42612
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2437 <BIE>
A:Cross-references: UNIPROT:P46530; UNIPARC:UPI000013056E; EMBL:X69088; NID:G433866; PID
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:755-786/Domain: EGF homology <EGF1>
F:1023-1054/Domain: EGF homology <EGF2>
F:1185-1216/Domain: EGF homology <EGF2>
F:1915-1947/Domain: ankyrin repeat homology <AN1>
F:1948-1980/Domain: ankyrin repeat homology <AN2>
F:1982-2014/Domain: ankyrin repeat homology <AN3>
F:2015-2047/Domain: ankyrin repeat homology <AN4>
F:2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 5.3%; Score 114; DB 2; Length 2437;
Best Local Similarity 19.2%; Pred. No. 0.66; Mismatches 159; Indels 112; Gaps 22;
Matches 77; Conservative 54; Mismatches 159; Indels 112; Gaps 22;

Qy 39 NSCTQARKKCE--ANPACKAAYQHLGSCSSLSRPLPLEESAMGADCLAEAEQLR-NSSL 95
| | | | |
Db 406 SACNQDIDECISLANPC-----EHGGRCLNT-----KGSFQCKCLQGYEGPRCEMDV 452
| | | | |
Qy 96 IDCRRMRMKHOATCLDIYWTVHPARSLGDYELDVSP-YE-----DVTISKPKWKN- 145
| | | | |
Db 453 NECKSN-PCQNDATCLD-----QIGGFHCICMPGYEVFCQINSDDCASQPC-LNG 501
| | | | |
Qy 146 --LSKLN-----MLKPSDLCL-----KFAMLCT-----LHD 170
| | | | |
Db 502 KCIDKINSFHCEPKFGSGSLCQVDVDECASTPCKNAGAKCTDGNPKYTCCTPGFSGIHC 561
| | | | |
Qy 171 KCDRLKAYGACSGIRCORHLCLLAQLRSF-----FEKAAESHAQGLLLCPCAPEDA 222
| | | | |
Db 562 ELDI-----NECASSPCHYGCDGVASFCTDCRPGYTGRLCETNINECLSQPC--RNG 613
| | | | |
Qy 223 CGGERRNTIAPSCALPSPVTPNCLDLRSFCRADPL-----CRSLMDPQTHCHPMDILGTC 278
| | | | |
Db 614 GTCQDRENAVICTCPKGTGTVNCEINIDDCRKPCKDYKCKIDKINGECVCEPGYSGMC 673
| | | | |
Qy 279 ATEQSRCLRAYLGLIGTAMTP-----NFISKVNTTVALSCTCRSGNQLQDECEQLERSFS 333
| | | | |
Db 674 NINIDDC-----ALNPNCHNGGTCTDGNW----SFTCLC-PDGFPRDATCLSQHNECS 719
| | | | |
Qy 334 QNPCLVEAIAAKRPHRQLFSQDWADSTFSV-VQOQNSNPAL 374
| | | | |
Db 720 SNFCHGSLCQDQINSYRCVCEAGWGMGRNCDININECLSNPCV 761
| | | | |

RESULT 12

A24420
notch protein - fruit fly (Drosophila melanogaster)
N:Alternate names: neurogenic repetitive locus protein
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: A24420; A24768; S09358; A05267
R:Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A:Reference number: A24420; MUID:87064624; PMID:3097517
A:Accession: A24420
A:Molecule type: DNA
A:Residues: 1-2703 <KID>
A:Cross-references: UNIPROT:P07207; UNIPARC:UPI000016BC06; GB:K03508; NID:G157991; PIDN
R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A:Reference number: A24768; MUID:86079539; PMID:3935325
A:Accession: A24768
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958

A;Cross-references: UNIPARC:UPI0000173D1F
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R;Tautz, D.
Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA markers
A;Reference number: S09358; MUID:89385974; PMID:2780284
A;Accession: S09358
A;Molecule type: DNA
A;Residues: 2505-2551, 'OQQQ', 2552-2576, 'E', 2578-2604 <TAU>
A;Cross-references: UNIPARC:UPI0000173D20
R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
A;Reference number: A05267; MUID:85099329; PMID:2981631
A;Accession: A05267
A;Molecule type: DNA
A;Residues: 2504-2576, 'E', 2578-2611 <WHA2>
A;Cross-references: UNIPARC:UPI0000173D21
C;Genetics:
A;Gene: notch; opa
A;Cross-references: FlyBase:FBgn0004647
A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-43/Domain: transmembrane #status predicted <TMW1>
F;297-328/Domain: EGF homology <EGX1>
F;530-561/Domain: EGF homology <EGP1>
F;568-599/Domain: EGF homology <EGP>
F;988-1019/Domain: EGF homology <EGX2>
F;1064-1095/Domain: EGF homology <EGF3>
F;1187-1218/Domain: EGF homology <EGX3>
F;1746-1762/Domain: transmembrane #status predicted <TMW2>
F;1950-1982/Domain: ankyrin repeat homology <AN1>
F;1983-2015/Domain: ankyrin repeat homology <AN2>
F;1988-2004/Domain: transmembrane #status predicted <TMW3>
F;2017-2049/Domain: ankyrin repeat homology <AN3>
F;2050-2082/Domain: ankyrin repeat homology <AN4>
F;2083-2115/Domain: ankyrin repeat homology <AN5>
F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 5.3%; Score 112.5; DB 1; Length 2703;
Best Local Similarity 21.6%; Pred. No. 0.98;
Matches 76; Conservative 34; Mismatches 127; Indels 115; Gaps 20;

QY 40 SCTQARKKCEANPACKAAAYQHLS-----CTSSLRPLPLESAMSADCLAEAEQLRNS 93
Db 1056 NCQYKLNKDSNPCLNGATCHEQNEVYTHCPSGFT-----GKQCSEYVDWCGQS 1105
QY 94 SLIDCRCHRRMKHQATC-LDIYTVHPARSLGDYELDVSPYEDTVTSKPKMNLKLNML 152
Db 1106 PCENGATCSQMKGFQSKCSAGWT----- 1129
QY 153 KPDSDLCLFAMLCITLHDKCDR-----LR-----KAYGEA-----CS-----GIRCORHL 192
Db 1130 ---GKLCVDTTISC-QDAADRKGLSLRQLCNGNCTKDYGNHVCYCSQGVAGSYCQKEI 1184
QY 193 --CLAQ-----LRSPFEKAEASHAQ-----LLLCFCAP---EDAG-CGERRNTI 232
Db 1185 DECSQPCQNGTGCTRDILIGAYECQCRQGFQNGELNIDPCANPNCGGTCHDRVNNF- 1243
QY 233 APSCALPSVTPNCL-----DLR-SFCRADPLCHRSRLMDFTQCHPMDILGTCAEQSRC 285
Db 1244 --SCSCPPTGTWGLICEINKDDCKGACHNNGSCIDRVGGFCVQCQPFVGAECBGDINEC 1301
QY 286 LRAYLGLIGTAMPNFIISKVNTTVALSCTCRSGNGLQDECEQLERSFSQNPC 337
Db 1302 LSNPCSNAGTL---DCVQLVNN---YHCNCR-PGHMGRHCEHKVDYFCAQSPC 1346

RESULT 13
S62935

hypothetical protein YNL023c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N2812
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
A;Accession: S62935; S62945
R;Andre, B.; Iraqi Housaini, I.; Urrestarazu, L.A.; Visser, S.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62920
A;Accession: S62935
A;Molecule type: DNA
A;Residues: 1-965 <AND>
A;Cross-references: UNIPROT:P53971; UNIPARC:UPI0000053082; EMBL:Z711299; NID:gl301854; P;
A;Experimental source: strain S288C
R;Duesterhoft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Accession: S62945
A;Molecule type: DNA
A;Residues: 1-965 <DUE>
A;Cross-references: UNIPARC:UPI0000053082; EMBL:Z711299; NID:gl301854; PID:6239870; PID;
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:FAP1
A;Cross-references: SGD:S0004968
A;Map position: 14L

Query Match 5.2%; Score 110; DB 2; Length 965;
Best Local Similarity 22.1%; Pred. No. 0.54; Mismatches 100; Indels 144; Gaps 22;
Matches 77; Conservative 28;

QY 42 TQARKKC-EANPACKAAAYQHLSCTSSL-----SRPLPLESAMSADCLAEAEQ 89
Db 339 TKPRKCHCDPIPTCDS-----RCGPKLCKGKHSPTCHDKACMEPLQIDSVKCAEQ 392
QY 90 -----LRNSSLIDCRCHRRMKHQATCLDIYTVHPARSLGDYELDVSPY 133
Db 393 STFSVPCGFGQRPNCNIKESLMSRRHR-----CTDRCCSGRP----- 431
QY 134 EDTVTSKPKMNLKLNMLKPD-----DLCLK-----FAMLCITLHDKCDRLRKAYGEACSG 185
Db 432 ----SATTRKKNLFRTQDLDLSLVEAKHICLPCNLTLSGGIH-KQR-----KCHP 479
QY 186 IRCORHLCLAQRSFFEKAAESHAQGLLCP-----APEDAGCGERRNTIAPSCALPSV 241
Db 480 GKCPP-CL-----ESDND-LVCPGCGTVVPAPVRCG-----TKLPTCNHPCI 520
QY 242 TPNCLDLRSPRADPLCRSLMDFTQCHPMDILGTCAEQSRCRLRAYLGLIGTAMP-- 299
Db 521 -----KVVRGEGSTCGHKMPHT--CHSLDVSCPECTE-----TVFKPK 557
QY 300 -NFISKVNTT---VALSC-----TCRSGNGLQDECEQ 327
Db 558 CGKTKRTVTCFTDVSQCGIKGCIPLSYCHTQKTCILPNCQKVKCK 606

RESULT 14
T18355

hypothetical protein P3 - Mycoplasma hyorhinis

C;Species: Mycoplasma hyorhinis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T18355
R;Deng, G.; McIntosh, M.A.
J. Bacteriol. 176, 5929-5937, 1994
A;Title: An amplifiable DNA region from the Mycoplasma hyorhinis genome.
A;Reference number: Z18888; MUID:95014025; PMID:7928953
A;Accession: T18355
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1187 <DEN>
A;Cross-references: UNIPROT:Q49549; UNIPARC:UPI00000B9898; EMBL:L11447; NID:gl50156; P;
C;Genetics:
A;Genetic code: SGCS

Query Match 5.2%; Score 110; DB 2; Length 1187;
Best Local Similarity 18.8%; Pred. No. 0.67; Mismatches 116; Indels 126; Gaps 20;
Matches 65; Conservative 38; Mismatches 116; Indels 126; Gaps 20;
QY 41 CTQARRKCEANPACAAAYQHLGSGCTSS---LSRPL-----PLEESAMADCL 84
DB 221 CANSKNVDCLESCN-----GQNEQIIVVKEPVQELPEEQATPEQIELTDLDDHF 274
QY 85 EAAEQLRNSLIDCRCHRRMKHQATC-----LDIYVTHVPARSLGVDYELDVSPYEDT 136
DB 275 ETV-HLEEEVCLAC-----QHVATCDICKNLSHSEILYRLKNGQVVNLLTELETEELH 327
QY 137 VTSKPKWMLSKLNLKPDSDCLKPFAMLCCL---HDKCDRLRKAYGEACSGIRCORHLC 193
DB 328 YADSP-----VOEGKEPC-----GCSLKETESCD-----CEACKQCEBNC 366
QY 194 LAQLRSFFKAEARSHAQGLLCLCAPEDAGCGRRRRNTIAPSCALPSVT-----PNCL 246
DB 367 CSELTGCGQEA-----CSCAQEHCGQEE-----SCACPNTTCACTEEHCECT 410
QY 247 DLRSFRCADPL-CRSRLMD-FQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFI 304
DB 411 ESTCGCENEPCEEEACDCSEHCE-----CVDETOACL-----D 446
QY 305 VNT---TVALSC-----TCRSGNQLQDECEQLERSFSQNPCLAVE 340
DB 447 CNTQADTKVCGCTQEQHPTC-----EECKECDECKQCKACLVQ 484

RESULT 15
S78549
notch3 protein - human
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S78549; S71825
R;Joutel, A.; Tournier-Lasserre, E.
submitted to the EMBL Data Library, April 1997
A;Reference number: S78549
A;Accession: S78549
A;Molecule type: mRNA
A;Residues: 1-2321 <JOU1>
A;Cross-references: UNIPROT:Q9UM47; UNIPARC:UPI000011D827; EMBL:U97669; NID:g2668591; PI
R;Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowit
x, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.
Nature 383, 707-710, 1996
A;Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
A;Reference number: S71825; PMID:97032728; PMID:8878478
A;Accession: S71825
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888 <JOU2
A;Cross-references: UNIPARC:UPI0000177457; UNIPARC:UPI0000177458; UNIPARC:UPI0000177459;
C;Genetics:
A;Gene: notch3
A;Map position: 19p13.1
C;Function:
A;Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: tandem repeat; transmembrane protein
F;123-155/Domain: EGF homology <EGX1>
F;162-194/Domain: EGF homology <EGF1>
F;240-271/Domain: EGF homology <EGX2>
F;318-349/Domain: EGF homology <EGF>
F;473-504/Domain: EGF homology <EGX3>
F;853-884/Domain: EGF homology <EGF3>
F;928-959/Domain: EGF homology <EGX4>
F;1838-1870/Domain: ankyrin repeat homology <AN1>
F;1871-1903/Domain: ankyrin repeat homology <AN2>
F;1905-1937/Domain: ankyrin repeat homology <AN3>
F;1938-1970/Domain: ankyrin repeat homology <AN4>
F;1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 5.2%; Score 110; DB 2; Length 2321;

Best Local Similarity 22.1%; Pred. No. 1.3;
Matches 78; Conservative 35; Mismatches 150; Indels 90; Gaps 21;
QY 41 CTQARRKCEANPACAAAYQHLGSGCTSSLSRPLPLEESAMADCLAEAEQLRNSLID-CR 99
DB 542 CDRNVDDCSPDPC-----HHGRCVDGI-----ASFSCACAPGYTGTTRCESQVDECR 587
QY 100 CHRRMKHQATCLDI---YVTHVPARSLG-DYELDVSPYEDT VTSKPKWMLSKLNLKPKD 155
DB 588 -SOPCRHGGKCLDLVDKYLRCRCPSGTGTGVNCEVNI-----DDCASNPCTFGVCRDGINRYD 642
QY 156 SDCLCK--FAMLCCTLH-DKCDRLRKAYGEAC---SGIRC-----QRHLCLAQLRSFFE 202
DB 643 C-VCQPGFTGPLCNVEINECASSPCGEGGSCVDGNGFRCCLCPGSLPLPCLPPSHPCA 701
QY 203 KAAESH-----AOGLLLCPCAPEDAGCGRRRRNTIAPSCALPSVTNCLDLRSFCADPL 257
DB 702 EPC-SHGICYDAPGGFRVCVCEFGWSG-----PRCSQSLARDACES--QPCRAGGT 748
QY 258 CRSRLMDFOHCHP-----MDILGTCA-----EQSRCL 286
DB 749 CSSDGMGFHCTCPPGVQGRQCELLSPCTNPCEHGGRCESAPGQLPVCSPQGWQGRPCQ 808
QY 287 RAYLGLIGTA-MTPNPFISKVNTTVALSCTCRSGNQLQDECEQLERSFSQNPCL 338
DB 809 QDVDECAGFAPCGPHGIC-TNLGSGFSCTCHG-GYTGPSCDODINDCDENPCL 859

Search completed: May 12, 2006, 02:10:30
Job time : 27.404 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:00:03 ; Search time 152.922 Seconds
(without alignments)
1831.616 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPILSFLPILLLQLTLW 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	1	GFR33_MOUSE
2	2058	96.6	385	2	Q9R2D0_MOUSE
3	1972	92.5	397	2	Q6AXR3_RAT
4	1646.5	77.3	400	1	GFR33_HUMAN
5	1167	54.8	222	2	Q9Q2G2_RAT
6	581.5	27.3	465	1	GFR22_CHICK
7	577.5	27.1	444	2	Q792X9_RAT
8	577.5	27.1	464	2	Q5B9X0_BOVIN
9	577.5	27.1	464	2	Q35977_RAT
10	576.5	27.1	463	1	GFR22_MOUSE
11	576.5	27.1	463	2	Q920V3_MOUSE
12	574.5	27.0	460	2	Q5R229_PONPY
13	574.5	27.0	464	1	GFR22_HUMAN
14	574.5	27.0	464	2	Q6GTR9_HUMAN
15	574.5	27.0	464	2	Q5RAD6_PONPY
16	564.5	26.5	464	2	Q5R9T3_PONPY
17	531	24.9	469	1	GFR11_CHICK
18	519	24.4	495	2	Q6TSC3_BRARE
19	514.5	24.1	481	2	Q9RTF8_BRARE
20	513.5	24.1	465	1	GFR11_HUMAN
21	513	24.1	472	2	Q98TT9_BRARE
22	510	23.9	463	2	Q35252_MOUSE
23	508.5	23.9	468	1	GFR11_MOUSE
24	508.5	23.9	468	2	Q35246_MOUSE
25	507	23.8	431	2	Q4R568_TETNG
26	507	23.8	463	2	Q35748_RAT
27	505.5	23.7	468	1	GFR11_RAT
28	490	23.0	431	1	GFR11_CHICK
29	489.5	23.0	484	2	Q4SIR4_TETNG
30	468.5	22.0	333	2	Q4RTG0_TETNG
31	442.5	20.8	358	2	Q922A3_MOUSE

32	436.5	20.5	359	2	Q58J92_HUMAN	Q58j92 homo sapien
33	429.5	20.2	342	2	Q4SDM1_TETNG	Q4sdm1 tetraodon n
34	429	20.1	330	2	Q922A2_MOUSE	Q922a2 mus musculus
35	412	19.3	203	2	Q4SF7_TETNG	Q4sf7 tetraodon n
36	375.5	17.6	260	1	GFR44_MOUSE	Q9jft2 mus musculus
37	371	17.4	273	1	GFR44_RAT	Q9ep12 rattus norv
38	294	13.8	299	1	GFR44_HUMAN	Q9gzz7 homo sapien
39	294	13.8	299	2	Q5JT74_HUMAN	Q5jt74 homo sapien
40	272.5	12.8	247	2	Q4SG83_TETNG	Q4sg83 tetraodon n
41	264.5	12.4	182	2	Q5JT77_HUMAN	Q5jt77 homo sapien
42	232	10.9	394	2	Q6UXV0_HUMAN	Q6uxv0 homo sapien
43	223.5	10.5	333	2	Q6SJE0_MOUSE	Q6sj60 mus musculus
44	204	9.6	223	2	Q9QWK2_MOUSE	Q9qw22 mus musculus
45	199.5	9.4	109	2	Q8JG58_AMBME	Q8jg58 ambystoma m

RESULT 1

GFR33_MOUSE STANDARD; PRT; 397 AA.

ID GFR33_MOUSE O55243; O6NZC2; Q8C8L9;

AC O35118; O35325; O55243; O6NZC2; Q8C8L9;

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Theria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

GN GFR33_MOUSE

LN Nucleotide sequence

RC STRAIN=C57BL/6; TISSUE=Heart;

RX MEDLINE=98205811; PubMed=9535755; DOI=10.1006/bbrc.1998.8361;

RA Nomoto S., Ito S., Yang L.-X., Kiuchi K.;

RT "Molecular cloning and expression analysis of GFR alpha-3, a novel cDNA related to GDNF alpha and NTR-alpha."

RL Biochem. Biophys. Res. Commun. 244:849-853(1998).

RN Nucleotide sequence.

RP MEDLINE=98420233; PubMed=9749804;

RA Widenfalk J., Tomac A., Lindqvist E., Hoffer B., Olson L.;

RT "GFRalpha-3, a protein related to GFRalpha-1, is expressed in developing peripheral neurons and ensheathing cells."

RL Eur. J. Neurosci. 10:1508-1517(1998).

RN Nucleotide sequence.

RP PubMed=9448325; DOI=10.1073/pnas.95.3.1295;

RA Naveilhan P., Baudet C., Mikaelis A., Shen L., Westphal H., Ernfore P.;

RT "Expression and regulation of GFRalpha3, a glial cell line-derived neurotrophic factor family receptor."

RL Proc. Natl. Acad. Sci. U.S.A. 95:1295-1300(1998).

RN Nucleotide sequence.

RP MEDLINE=98245162; PubMed=9576965; DOI=10.1073/pnas.95.10.5801;

32	436.5	20.5	359	2	Q58J92_HUMAN	Q58j92 homo sapien
33	429.5	20.2	342	2	Q4SDM1_TETNG	Q4sdm1 tetraodon n
34	429	20.1	330	2	Q922A2_MOUSE	Q922a2 mus musculus
35	412	19.3	203	2	Q4SF7_TETNG	Q4sf7 tetraodon n
36	375.5	17.6	260	1	GFR44_MOUSE	Q9jft2 mus musculus
37	371	17.4	273	1	GFR44_RAT	Q9ep12 rattus norv
38	294	13.8	299	1	GFR44_HUMAN	Q9gzz7 homo sapien
39	294	13.8	299	2	Q5JT74_HUMAN	Q5jt74 homo sapien
40	272.5	12.8	247	2	Q4SG83_TETNG	Q4sg83 tetraodon n
41	264.5	12.4	182	2	Q5JT77_HUMAN	Q5jt77 homo sapien
42	232	10.9	394	2	Q6UXV0_HUMAN	Q6uxv0 homo sapien
43	223.5	10.5	333	2	Q6SJE0_MOUSE	Q6sj60 mus musculus
44	204	9.6	223	2	Q9QWK2_MOUSE	Q9qw22 mus musculus
45	199.5	9.4	109	2	Q8JG58_AMBME	Q8jg58 ambystoma m

ALIGNMENTS

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skolala U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
CC factor, artemin. Mediates the artemin-induced autophosphorylation
CC and activation of the RET receptor tyrosine kinase (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: Belongs to the GDNFR family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB008833; BAA23562.1; -; mRNA.
DR EMBL; AF041842; AAC23558.1; -; mRNA.
DR EMBL; AF036163; AAC24468.1; -; mRNA.
DR EMBL; AF051766; AAC24354.1; -; mRNA.
DR EMBL; AF020305; AAB70931.1; -; mRNA.

DR EMBL; AK046542; BAC32778.1; -; mRNA.
DR EMBL; BC066202; AAH66202.1; -; mRNA.
DR PIR; J00082; JE0082.
DR Ensemble; ENSMUSG00000024366; Mus musculus.
DR MGI; MGI:1201403; Gira3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; F:axon guidance; IMP.
DR GO; GO:0007422; P:peripheral nervous system development; IMP.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR PANTHER; PTHR10269; GDNF_receptor; 1.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
DR Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
KW SIGNAL 1 28 Potential.
FT CHAIN 29 371 GDNF family receptor alpha 3.
FT PROPEP 372 397 Removed in mature form (Potential).
FT LIPID 371 GPI-anchor amidated asparagine (Potential).
FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 306 306 N-linked (GlcNAc...) (Potential).
FT CONFLICT 5 6 WS -> LE (in Ref. 2 and 3).
FT CONFLICT 66 66 S -> C (in Ref. 6).
FT CONFLICT 218 218 A -> P (in Ref. 2, 3 and 5).
FT CONFLICT 314 314 T -> S (in Ref. 7).
SQ SEQUENCE 397 AA; 44307 MW; BB66CEP65D32A4B9 CRC64;
Query Match 100.0%; Score 2131; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.7e-171;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
DB 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
QY 61 LGSCTSSLSRPLPLESAMSADCLEAQLRNSSLIDCRCHRMKHQATCLDIYTVTHPA 120
DB 61 LGSCTSSLSRPLPLESAMSADCLEAQLRNSSLIDCRCHRMKHQATCLDIYTVTHPA 120
QY 121 RSLGDIYELDVSPYETVTSKPKWNLKMLKPSDLCKEAMCTLDKCDRLRKAYG 180
DB 121 RSLGDIYELDVSPYETVTSKPKWNLKMLKPSDLCKEAMCTLDKCDRLRKAYG 180
QY 181 EACSGIRCORHLCLLAQLRSFFFEKAASHAQGLLLCPACEDAGCGERRNTIAPSCALPS 240
DB 181 EACSGIRCORHLCLLAQLRSFFFEKAASHAQGLLLCPACEDAGCGERRNTIAPSCALPS 240
QY 241 VTPNCLDLRSFCRADPLCRSLRMDFTQCHPMIDILGTCAEQSRCLRAYLGLIGTAMTNP 300
DB 241 VTPNCLDLRSFCRADPLCRSLRMDFTQCHPMIDILGTCAEQSRCLRAYLGLIGTAMTNP 300
QY 301 FISKVNTTVALSCTCGSNLODECEQLERSFSONPCLVEATAAKMRPHRQLPSQDWADS 360
DB 301 FISKVNTTVALSCTCGSNLODECEQLERSFSONPCLVEATAAKMRPHRQLPSQDWADS 360
QY 361 TFSVQQQNSNPALRLQPLRPILSPSILPLILLQTLW 397
DB 361 TFSVQQQNSNPALRLQPLRPILSPSILPLILLQTLW 397
RESULT 2
Q9R2D0_MOUSE PRELIMINARY; PRT; 385 AA.
ID Q9R2D0_MOUSE
AC Q9R2D0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE TGF-beta-related neurotrophic receptor-3 precursor.
GN Name=Gfra3; Synonyms=TrnR-3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Swiss-Webster
RA Zhong J., Annie M., Tolle A., Heumann R.;
RT "Molecular cloning of a new member of TrnR family";
RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15110; CAA75384.1; -; mRNA.
DR MGI; MGI:1201403; Gfra3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; F:axon guidance; IMP.
DR GO; GO:0007422; P:peripheral nervous system development; IMP.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor; Signal.
FT SIGNAL 1 15 Potential.
SQ SEQUENCE 385 AA; 42997 MW; 91A7F3F9FF30ED14 CRC64;

Query Match 96.6%; Score 2058; DB 2; Length 385;
Best Local Similarity 99.7%; Pred. No. 5.2e-165;
Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 MILLVLSLWLPGLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCSTSSLSRPL 72
Db 1 MILLVLSLWLPGLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCSTSSLSRPL 60

Qy 73 PLESAMSDCLEAAEQRLNSLIDCRCHRMKHOATCLDIYVTVHPARSLGVDYELDVSP 132
Db 61 PLESAMSDCLEAAEQRLNSLIDCRCHRMKHOATCLDIYVTVHPARSLGVDYELDVSP 120

Qy 133 YEDTVTSKPKWNLKSLNMLKPSDCLCKFAMLTCLHDKCDRLKAYGEACSGIRCQRL 192
Db 121 YEDTVTSKPKWNLKSLNMLKPSDCLCKFAMLTCLHDKCDRLKAYGEACSGIRCQRL 180

Qy 193 CLAQLRSFFFEKAESHAQGLLLCPAPEDAGCGRRNTTAPSCALPSVTPNCLDLRSFC 252
Db 181 CLAQLRSFFFEKAESHAQGLLLCPAPEDAGCGRRNTTAPSCALPSVTPNCLDLRSFC 240

Qy 253 RADPLCSRLMDFQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTNPFSKNTTVALS 312
Db 241 RADPLCSRLMDFQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTNPFSKNTTVALS 300

Qy 313 CTCRGSNLDCEQLRSFQNPCLVEAIAAKRFRHQLFSQDWDSTFVVQQQNSP 372
Db 301 CTCRGSNLDCEQLRSFQNPCLVEAIAAKRFRHQLFSQDWDSTFVVQQQNSP 360

Qy 373 ALRLQPLRLPILSPILPILLOTI 397
Db 361 ALRLQPLRLPILSPILPILLOTI 385

RESULT 3
Q6AXR3 RAT PRELIMINARY; PRT; 397 AA.
ID Q6AXR3 RAT
AC Q6AXR3
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Gial cell line derived neurotrophic factor family receptor alpha 3.

GN Name=Gfra3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RC NIH MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079378; AAH79378.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 397 AA; 44053 MW; E11D2E7B9CB46AF8 CRC64;

Query Match 92.5%; Score 1972; DB 2; Length 397;
Best Local Similarity 92.9%; Pred. No. 9.6e-158;
Matches 369; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGLSWSRPPPLMLILLVLSLWLPGLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
Db 1 MGLSWSRPPPLMLILLVLSLWLPGLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy 61 LGSCTSSLSRPLPLESAMSADCLEAAEQRLNSLIDCRCHRMKHOATCLDIYVTVHPA 120
Db 61 LDSCPTSSLSPLSGESATSAACLEAAEQRLNSLIDCRCHRMKHOATCLDIYVTVHPV 120

Qy 121 RSLGDIYELDVSPYEDTVTSKPKWNLKSLNMLKPSDCLCKFAMLTCLHDKCDRLKAYG 180
Db 121 RSLGDIYELDVSPYEDTVTSKPKWNLKSLNMLKPSDCLCKFAMLTCLHDKCDRLKAYG 180

Qy 181 EACSGIRCQRLCLAQRLSFFFEKAESHAQGLLLCPAPEDAGCGRRNTTAPSCALPS 240
Db 181 EACSGIRCQRLCLAQRLSFFFEKAESHAQGLLLCPAPEDAGCGRRNTTAPSCALPS 240

Qy 241 VTPNCLDLRSFCRADPLCSRLMDFQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTNP 300
Db 241 VAPNCLDLRSFCRADPLCSRLMDFQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTNP 300

Qy 301 FISKVNTTVALSCTCRGSNLDCEQLRSFQNPCLVEAIAAKRFRHQLFSQDWDSTF 360
Db 301 FISKVNTTVALGCTCRGSNLDCEQLRSFQNPCLVEAIAAKRFRHQLFSQDWDSTF 360

QY 361 TFSVVOQNSPALRLOPLRPLSPILPILLOTLW 397
 DB 361 TFSVMOQNSPALRPLRPLVLPFILTLLOTLW 397

RESULT 4

GFR3A3_HUMAN
 ID GFR3A3_HUMAN STANDARD; PRT; 400 AA.
 AC O60609; Q6UW20; Q8RU22;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).
 GN Name=GFR3A3; ORFNames=UNQ339/PRO538/PRO3664;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE (ISOFORM 1), AND TISSUE SPECIFICITY.
 RP MEDLINE=98245162; PubMed=9576965; DOI=10.1101/gr.1293003;
 RX Baloh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,
 RA Popeacu N.C., Johnson E.M. Jr., Milbrandt J.;
 RT "GFRalpha3 is an orphan member of the GDNF/neurturin/persephin
 receptor family";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806 (1998).
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
 RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment";
 RL Genome Res. 13:2265-2270(2003).
 [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RP TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RN PROTEIN SEQUENCE OF 32-46.
 RP PubMed=15340161; DOI=10.1110/ps.04682504;
 RX Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 verified cleavage sites";

RL Protein Sci. 13:2819-2824 (2004).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=99098192; PubMed=9883723; DOI=10.1016/S0896-6273(00)80649-2;
 RA Baloh R.H., Tansey M.G., Lampe P.A., Fahrner T.J., Enomoto H.,
 RA Simburger K.S., Leitner M.L., Araki T., Johnson E.M. Jr.,
 RA Milbrandt J.;
 RT "Artemin, a novel member of the GDNF ligand family, supports
 peripheral and central neurons and signals through the GFRalpha3-RET
 receptor complex";
 RL Neuron 21:1291-1302(1998).
 CC -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
 factor, artemin. Mediates the artemin-induced autophosphorylation
 and activation of the RET receptor tyrosine kinase.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O60609-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O60609-2; Sequence=VSP_010942;
 CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetus which
 exhibit a similar pattern. Essentially not expressed in the
 central nervous system, but highly expressed in several sensory
 and sympathetic ganglia of the peripheral nervous system. Moderate
 expression in many nonneural tissues, particularly those of the
 digestive and urogenital systems, but high expression in stomach
 and appendix. Several types of glandular tissues show low
 expression. Very low or no expression detected in the
 hematopoietic system.
 CC -!- SIMILARITY: Belongs to the GDNFR family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL; AF051767; AAC24355.1; -; mRNA.
 DR EMBL; AY358997; AAQ89356.1; -; mRNA.
 DR EMBL; AY359037; AAQ89396.1; -; mRNA.
 DR EMBL; BC037951; AAH37951.1; -; mRNA.
 DR Ensembl; ENSG0000146013; Homo sapiens.
 DR HGNC; HGNC:4245; GFR3A3.
 DR MIM; 605710; -;
 DR GO; GO:0019898; C:extrinsic to membrane; TAS.
 DR GO; GO:0005102; F:receptor binding; TAS.
 DR GO; GO:0007422; P:peripheral nervous system development; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR003438; GDNF_receptor.
 DR InterPro; IPR003505; GDNF_receptorA3.
 DR PANTHER; PTHR10269; GDNF_receptor; 1.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01319; GDNFRALPHA3.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;
 KW GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 374 GDNF family receptor alpha 3.
 FT PROPEP 375 400 Removed in mature form (Potential).
 FT LIPID 374 374 GPI-anchor amidated asparagine
 (Potential).
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc...) (Potential).
 FT VARSPIC 127 157 Missing (in isoform 2).
 FT /FTId=VSP_010942.
 FT CONFLICT 108 108 K -> R (in Ref. 1).
 FT SEQUENCE 400 AA; 44511 MW; B0BC252FE1F072C7 CRC64;
 Query Match 77.3%; Score 1646.5; DB 1; Length 400;
 Best Local Similarity 77.8%; Pred. No. 2.7e-130;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENFVNSCTQARKKCBANPACKAAYQHLAGSCT 65
 DB 9 PLPPVWMLLLPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAYHLDSC 68
 QY 66 SSLSRPLPESAMSADCLAEABQLRNSLLIDCHRRMKQATCLDIYTWVHPARSLGD 125
 DB 69 SSITPLPSEEPSPADCLAEAAQQLRNSLLIGCMCHRRMKQVACLDIYTWVHARSIGN 128
 QY 126 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLDKCDRLRKAYGEACSG 185
 DB 129 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLDKCDRLRKAYGEACSG 188
 QY 186 IRCORHLCLAQRLRSFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSPVNC 245
 DB 189 PHCQRHVLCRLQTLTFFKAAEPHAQGLLLCPAPEDAGCGERRNTIAPNCALPPVAPNC 248
 QY 246 LDLSRPFCEADPLCRSRLMDPQTHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSKV 305
 DB 249 LELRLCFSDPLCRSRLVDFQTHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSNV 308
 QY 306 NTTVALSCTCRGSGNLODECQLERSFSONPCLVEATAAKWRFHQLFSQDWDSTFSV 365
 DB 309 NTSVALSCTCRGSGNLODECQEMLEGGFHSNPNCLTEATAAKWRFHQLFSQDWDPTFAV 368
 QY 366 QQQNSPALRLQPLPILSILPILQLTLW 397
 DB 369 AHQENPAVRPQPVPSLFSCTLPLILLLSLW 400

RESULT 5
 Q9QZG2 RAT . PRELIMINARY; PRT; 222 AA.
 AC Q9QZG2;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE GDNF-family, receptor alpha 3 (Fragment).
 GN Name=Gfra3; Synonyms=GFRalpha-3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Cochlea;
 RX MEDLINE=20185640; PubMed=10719212; DOI=10.1016/S0169-328X(99)00328-9;
 RA Stover T., Gong T.L., Cho Y., Altschuler R.A., Lomax M.I.;
 RT "Expression of the GDNF family members and their receptors in the
 mature rat cochlea.";
 RL Brain Res. Mol. Brain Res. 76:25-35(2000).
 DR EMBL; AF184920; AAF01242.1; -; mRNA.
 DR Ensembl; ENSRNOG0000020309; Rattus norvegicus.
 DR RGD; 620502; Gfra3.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003438; GDNF receptor.
 DR InterPro; IPR003505; GDNF_receptorA3.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01319; GDNFRALPHA3.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 222 222
 SQ SEQUENCE 222 AA; 24791 MW; A9610F6462468C74 CRC64;

Query Match 54.8%; Score 1167; DB 2; Length 222;
 Best Local Similarity 96.4%; Pred. No. 3.8e-90;
 Matches 214; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 136 TVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLDKCDRLRKAYGEACSGIRCORHLCLA 195
 DB 1 TVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLDKCDRLRKAYGEACSGIRCORHLCLA 60

QY 196 QLRSFPEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSPVTPNCLDLRSFCRAD 255
 DB 61 QLRSFPEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSPVAPNCLDLRSFRAD 120
 QY 256 PLCRSRLMDPQTHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSKNTTVALSCTC 315
 DB 121 PLCRSRLMDPQTHCHPMDILGTCTEQSRCLRAYLGLIGTAMTNPFSKNTTVALGCTC 180
 QY 316 RGSNLODECQLERSFSONPCLVEATAAKWRFHQLFSQDW 357
 DB 181 RGSNLODECQLEKSPSNPCLMEATAAKWRFHQLFSQDW 222

RESULT 6
 GFRA2 CHICK STANDARD; PRT; 465 AA.
 ID GFRA2 CHICK
 AC O13157;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin
 receptor alpha) (NTRN-alpha) (NRTNR-alpha) (GDNF receptor beta)
 DE (GDNFR-beta).
 GN Name=GFRA2; Synonyms=GDNFRB;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archoeauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97336104; PubMed=9192899; DOI=10.1038/42729;
 RA Buj-Bello A., Adu J., Pinon L.G.P., Horton A., Thompson J.,
 RA Rosenthal A., Chinchetru M., Buchman V.L., Davies A.M.;
 RT "Neurturin responsiveness requires a GPI-linked receptor and the Ret
 receptor tyrosine kinase.";
 RL Nature 387:721-724(1997).
 CC -I- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced
 autophosphorylation and activation of the RET receptor. Also able
 to mediate GDNF signaling through the RET tyrosine kinase receptor
 (by similarity).
 CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -I- SIMILARITY: Belongs to the GDNFR family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL; U90542; AAB61571.1; -; mRNA.
 DR Ensembl; ENSGALG0000001795; Gallus gallus.
 DR InterPro; IPR003438; GDNF receptor.
 DR InterPro; IPR003504; GDNF_receptorA2.
 DR PANTHER; PTHR10269; GDNF_receptor; 1.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01318; GDNFRALPHA2.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 445
 FT PROPEP 445 465
 FT LIPID 445 445
 FT CARBOHYD 355 355
 FT CARBOHYD 387 387
 FT CARBOHYD 412 412
 SQ SEQUENCE 465 AA; 51909 MW; 22CD9024ED971F06 CRC64;

Query Match 27.3%; Score 581.5; DB 1; Length 465;
 Best Local Similarity 36.0%; Pred. No. 2.1e-40;
 Matches 130; Conservative 51; Mismatches 135; Indels 45; Gaps 11;
 QY 136 TVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLDKCDRLRKAYGEACSGIRCORHLCLA 195
 DB 1 TVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLDKCDRLRKAYGEACSGIRCORHLCLA 60

Db 40 CVRANELCAESNCSSRYRTLRQCLAGDRNTML-----ANKECOAALEVLQESPLYDCRC 95
Qy 101 HRRMKHQATCLDIYVTVHPARSLGVDYELDSVPYEDTVTSKPKWNLSKLNML----- 152
Db 96 KRGKKELQCLQIYWSIHLGLTEGEFEYASPYE-----PVTARLSDIPLASIFSGTG 149
Qy 153 -----KPSDILCLKPFAMCTLHDKCDRLRKAYGBACS-----GIRCQRHLCLAQLRSFFE 202
Db 150 ADPAVSTKSNHCLDAKACNLNDCKLRSSYISICNREISPTERCNRKCHKALRQFFD 209
Qy 203 KAASHAQGLLCCAPEDAGCGRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSEYTYRMLFCS-ODQACABRRQTLPLSCSYEDKEKPNCLDLRSCLRTDHLCKSR 267
Qy 262 LMDPQTHCH-PMDILGTGTCATQ-SRCLRAYLGLGTAMTNPFIISKVNTTVALS--CTCRG 317
Db 268 LADFHANCRAVYQTLTSCPTDNYOACLSYAGMIGFDITPNYDSSPTGIWVSPWCSCRG 327
Qy 318 SGNLQDECEQLERSFSQNPLVEAIAA 344
Db 328 SGNMECEKPLDFTENPCLRNAIOA 354

RESULT 9

O35977 RAT PRELIMINARY; PRT; 464 AA.
AC O35977;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Glial cell line-derived neurotrophic factor receptor-beta (RET ligand 2).
DE Name=Gfra2; Synonyms=GNFR-beta, RETL2;
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=98271460; PubMed=9608533; DOI=10.1006/mcne.1998.0667;
RA Trupp M., Raynoschek C., Belluardo N., Ibanez C.F.;
RT "Multiple GPI-anchored receptors control GDNF-dependent and independent activation of the c-ret receptor tyrosine kinase.";
RL Mol. Cell. Neurosci. 11:47-63(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain/kidney;
RX MEDLINE=97322356; PubMed=9177201; DOI=10.1073/pnas.94.12.6238;
RA Sanicola M., Hession C.A., Worley D.S., Carmillo P., Ehrenfels C., Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitty A., Pepinsky R.B., Cate R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
DR EMBL; AF005226; AAB62247.1; -; mRNA.
DR EMBL; U97143; AAC53301.1; -; mRNA.
DR Ensembl; ENSRNOG0000014010; Rattus norvegicus.
DR RGD; 61809; Gfra2.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 464 AA; 51668 MW; 81168301BE50D6CC CRC64;
Query Match 27.1%; Score 577.5; DB 2; Length 464;
Best Local Similarity 38.8%; Pred. No. 4.6e-40;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;
Qy 41 CTQARKKCEANPACKAAYQHLGCTSSLSRPLPLEBSAMSADCLAEAAQLRNSLIDCRC 100

Db 40 CVRANELCAESNCSSRYRTLRQCLAGDRNTML-----ANKECOAALEVLQESPLYDCRC 95
Qy 101 HRRMKHQATCLDIYVTVHPARSLGVDYELDSVPYEDTVTSKPKWNLSKLNML----- 152
Db 96 KRGKKELQCLQIYWSIHLGLTEGEFEYASPYE-----PVTARLSDIPLASIFSGTG 149
Qy 153 -----KPSDILCLKPFAMCTLHDKCDRLRKAYGBACS-----GIRCQRHLCLAQLRSFFE 202
Db 150 ADPAVSTKSNHCLDAKACNLNDCKLRSSYISICNREISPTERCNRKCHKALRQFFD 209
Qy 203 KAASHAQGLLCCAPEDAGCGRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSEYTYRMLFCS-ODQACABRRQTLPLSCSYEDKEKPNCLDLRSCLRTDHLCKSR 267
Qy 262 LMDPQTHCH-PMDILGTGTCATQ-SRCLRAYLGLGTAMTNPFIISKVNTTVALS--CTCRG 317
Db 268 LADFHANCRAVYQTLTSCPTDNYOACLSYAGMIGFDITPNYDSSPTGIWVSPWCSCRG 327
Qy 318 SGNLQDECEQLERSFSQNPLVEAIAA 344
Db 328 SGNMECEKPLDFTENPCLRNAIOA 354
RESULT 10
Gfra2 MOUSE STANDARD; PRT; 463 AA.
AC O08842;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin receptor alpha) (NTRN-alpha) (NRTNR-alpha) (TGF-beta related neurotrophic factor receptor 2) (GDNF receptor beta) (GDNFR-beta).
DE Name=Gfra2; Synonyms=cdnfrb, Trnr2;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RX MEDLINE=97325791; PubMed=9182803; DOI=10.1016/S0896-6273(00)80318-9;
RA Baloh R.H., Tansey M.G., Golden J.P., Creedon D.J., Heuckeroth R.O., Keck C.L., Zimonjic D.B., Popescu N.C., Johnson E.M. Jr., Milbrandt J.;
RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling through Ret.";
RL Neuron 18:793-802(1997).
CC -!- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced autophosphorylation and activation of the RET receptor. Also able to mediate GDNF signaling through the RET tyrosine kinase receptor.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=O08842-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=O08842-2; Sequence=VSP_001662;
CC -!- TISSUE SPECIFICITY: Neurons of the superior cervical and dorsal root ganglia, and adult brain and testis. Low level in the spleen and in the adrenal gland.
CC -!- SIMILARITY: Belongs to the GDNFR family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; AF002701; AAC53548.1; -; mRNA.

DR Ensembl; ENSMUSG0000022103; Mus musculus.
DR MGI; MGI:1195462; Gfra2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0007399; P:neurogenesis; IMP.
DR InterPro; IPR003438; GDNF receptor.
DR InterPro; IPR003504; GDNF receptorA2.
DR PANTHER; PTHR10269; GDNF_Receptor; 1.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PRO1318; GDNFRALPHA2.
DR PRINTS; PRO1316; GDNFRECEPTOR.
KW Alternative splicing; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
KW Receptor; Signal.
FT STGNAL 1 21 Potential.
FT CHAIN 22 443 GDNF family receptor alpha 2.
FT PROPEP 444 463 Removed in mature form (Potential).
FT LIPID 443 443 GPI-anchor amidated serine (Potential).
FT CARBOHYD 52 52 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 357 357 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 413 413 N-linked (GLCNAC. . .) (Potential).
FT VARSPLIC 14 146 Missing (in isoform 2).
FT FTId=VSP_001662.
SQ SEQUENCE 463 AA; 51599 MW; 4FB495FA58C61F78 CRC64;
Query Match 27.1%; Score 576.5; DB 1; Length 463;
Best Local Similarity 36.2%; Pred. No. 5.5e-40;
Matches 134; Conservative 45; Mismatches 138; Indels 53; Gaps 12;
QY 41 CTQARKKCEANPACKAAQYHLGSCSTSSLRPLPLEESAMSDCLEAAEQLRNSLLDRC 100
DB 40 CVRANELCAAESNCSSRYRTLQCLAGRDNTML-----ANKECQAALVLESPLYDCRC 95
QY 101 HRMKHQATCLDIYVTHVPARSLGYELDVSPYEDVTTSKPKWMLSKL----- 149
DB 96 KRGMKELQCLQIYWSIHGLTGEFEYASPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPSDCLCLFAMLCCTLDKCDRLRKAYGEACS-----GIRCORHLCLAQLRSFPE 202
DB 150 ADPVSAKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRKCHKALAQFDD 209
QY 203 KAASHAQGLLLCPCAPEDAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 210 RVPSEYTYRMLFCSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRLCRTLHLCSR 267
QY 262 LMDFOTHCHP--MDILGTCAEQSLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRG 317
DB 268 LADFHANCRAASYRTITSCPADNYQACLGSYAGMIGFMDTPNYVDSNPTGIIVSPWCNCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQF-----SQDWADSTFSVVOQNSN 371
DB 328 SGNMECEKFLKDFTEPNCLRNAI-----QAFNGTVDVNMSPKGPFFSATQA---- 375
QY 372 PALRLQPLRP 381
DB 376 PRVEKTPSLP 385

RESULT 11
Q920Y3_MOUSE PRELIMINARY; PRT; 463 AA.
AC Q920Y3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glial cell line derived neurotrophic factor family receptor alpha
DE 2.
GN Name=Gfra2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL;
RX MEDLINE=22712886; PubMed=12829325; DOI=10.1016/S0169-328X(03)00169-4;
RA Too H.P.;
RT "Real time PCR quantification of GFRalpha-2 alternatively spliced
isoforms in murine brain and peripheral tissues.";
RL Brain Res. Mol. Brain Res. 114:146-153(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL;
RC Wong Y.W., Too H.P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF398416; AAK97483.1; -; Genomic DNA.
DR EMBL; AF398411; AAK97483.1; JOINED; Genomic DNA.
DR EMBL; AF398412; AAK97483.1; JOINED; Genomic DNA.
DR EMBL; AF398414; AAK97483.1; JOINED; Genomic DNA.
DR EMBL; AF398415; AAK97483.1; JOINED; Genomic DNA.
DR EMBL; AF398417; AAK97483.1; JOINED; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PRO1318; GDNFRALPHA2.
DR PRINTS; PRO1316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 463 AA; 51582 MW; 42FAA1EF59975E2C CRC64;
Query Match 27.1%; Score 576.5; DB 2; Length 463;
Best Local Similarity 36.2%; Pred. No. 5.5e-40;
Matches 134; Conservative 45; Mismatches 138; Indels 53; Gaps 12;
QY 41 CTQARKKCEANPACKAAQYHLGSCSTSSLRPLPLEESAMSDCLEAAEQLRNSLLDRC 100
DB 40 CVRANELCAAESNCSSRYRTLQCLAGRDNTML-----ANKECQAALVLESPLYDCRC 95
QY 101 HRMKHQATCLDIYVTHVPARSLGYELDVSPYEDVTTSKPKWMLSKL----- 149
DB 96 KRGMKELQCLQIYWSIHGLTGEFEYASPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPSDCLCLFAMLCCTLDKCDRLRKAYGEACS-----GIRCORHLCLAQLRSFPE 202
DB 150 ADPVSAKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRKCHKALAQFDD 209
QY 203 KAASHAQGLLLCPCAPEDAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 210 RVPSEYTYRMLFCSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRLCRTLHLCSR 267
QY 262 LMDFOTHCHP--MDILGTCAEQSLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRG 317
DB 268 LADFHANCRAASYRTITSCPADNYQACLGSYAGMIGFMDTPNYVDSNPTGIIVSPWCNCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQF-----SQDWADSTFSVVOQNSN 371
DB 328 SGNMECEKFLKDFTEPNCLRNAI-----QAFNGTVDVNMSPKGPFFSATQA---- 375
QY 372 PALRLQPLRP 381
DB 376 PRVEKTPSLP 385
RESULT 12
Q5RE29_PONPY PRELIMINARY; PRT; 460 AA.
ID Q5RE29_PONPY
AC Q5RE29;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp4590181.
GN Name=DKFZp4590181;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Pongo.
OC NCBI_TaxID=9600;
RX NUCLEOTIDE SEQUENCE.


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FT CONFLICT 462 462 Q -> L (in Ref. 3).
SQ SEQUENCE 464 AA; 51559 MW; 8BC604D9530FF21F CRC64;

Query Match 27.0%; Score 574.5; DB 1; Length 464;
Best Local Similarity 37.9%; Pred. No. 8.2e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACKAAAYQHLSGCTSSLSRPLPLEESAMSADCLEAAEOLRNSSLIDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLROCLAGDRNTWL-----ANKCQAALVQLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYTWVHPARSLGDIYELDVSPYEDVTVTSKPWMNLSKL----- 149
DB 96 KRGMKKELQCLQIYWSIHLGLTGBEEFYEAAPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPDSDLLCKFAMLCITLHDKCDRLRKAYGEACS-----GIRCORHLCIAQLRSFPE 202
DB 150 ADPVVSAKSNHCLDAKACNLNDCKLRSSVISICNREISPTERCNRKCHKALRQFFD 209
QY 203 KAAESHAQGLLLCPCAPEDAGGERRRNTIAPSCAL-PSVTNCLDLRSFCRADPLCRSR 261
DB 210 RVPSEYTYRMLFCSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRGVCRTHLCSR 267
QY 262 LMDFOQHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFIKVNITVALS--CTCRG 317
DB 268 LADFHANCRASYQTVTSCPADNYQACLSYAGMIGDFTNPYVSDSPTGIVVSPWCSCRG 327
QY 318 SGNLQDECEQLRSFSONPCLVEAIAA 344
DB 328 SGNMBEBCFKFLRDTFNPCLRNAIOA 354

RESULT 14
Q6GTR9 HUMAN
ID Q6GTR9 HUMAN PRELIMINARY; PRT; 464 AA.
AC Q6GTR9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE GDNF family receptor alpha 2, preproprotein.
GN Name=GPR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Srapietko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
```

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RA Director MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041688; AAH41688.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 464 AA; 51543 MW; 8BC61529530FF21F CRC64;

Query Match 27.0%; Score 574.5; DB 2; Length 464;
Best Local Similarity 37.9%; Pred. No. 8.2e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACKAAAYQHLSGCTSSLSRPLPLEESAMSADCLEAAEOLRNSSLIDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLROCLAGDRNTWL-----ANKCQAALVQLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYTWVHPARSLGDIYELDVSPYEDVTVTSKPWMNLSKL----- 149
DB 96 KRGMKKELQCLQIYWSIHLGLTGBEEFYEAAPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPDSDLLCKFAMLCITLHDKCDRLRKAYGEACS-----GIRCORHLCIAQLRSFPE 202
DB 150 ADPVVSAKSNHCLDAKACNLNDCKLRSSVISICNREISPTERCNRKCHKALRQFFD 209
QY 203 KAAESHAQGLLLCPCAPEDAGGERRRNTIAPSCAL-PSVTNCLDLRSFCRADPLCRSR 261
DB 210 RVPSEYTYRMLFCSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRGVCRTHLCSR 267
QY 262 LMDFOQHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFIKVNITVALS--CTCRG 317
DB 268 LADFHANCRASYQTVTSCPADNYQACLSYAGMIGDFTNPYVSDSPTGIVVSPWCSCRG 327
QY 318 SGNLQDECEQLRSFSONPCLVEAIAA 344
DB 328 SGNMBEBCFKFLRDTFNPCLRNAIOA 354

RESULT 15
Q6RAD6 PONPY
ID Q6RAD6 PONPY PRELIMINARY; PRT; 464 AA.
AC Q6RAD6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459C0228.
GN Name=DKFZp459C0228;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RA Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR859081; CAH91274.1; -, mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01316; GDNFPRALPHA2.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51560 MW; 46441C50299CCCFA CRC64;

Query Match 27.0%; Score 574.5; DB 2; Length 464;
Best Local Similarity 37.9%; Pred. No. 8.2e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACKAAAYQHLSGCTSSLSRPLPLEESAMSADCLEAAEOLRNSSLIDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLROCLAGDRNTWL-----ANKCQAALVQLQESPLYDCRC 95
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Qy 101 HRRMKHQATCLDIYVTHPARSLGDEYLDVSPYEDVTTSKPKMNLKSL----- 149
Db 96 KRGKKELQCLQIYWSIHGLTEGEFFYEASPYB-PVTSR-----LSDIFELASIFSGTG 149
Qy 150 --NMLKPDSDLCLKPFAMCTLHDKCDRLRKAYGEACS-----GIRCORHLCLAOIRSFPE 202
Db 150 ADPVVSAKSNHCLDAAKACNLNDCKKLRSSYISICNREISPTERCNRRKCHKALRQFFD 209
Qy 203 KAESHAQGLLLCPCAPEDAGCGRRRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSEYTYRMLFCSC--ODQACERRRRTIIPSCSYEDKEKPNCLDLRGVCTDRLCRSR 267
Qy 262 LMDFTQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRG 317
Db 268 LADPHANCRAASYQTVTSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIWVSPWCSCRG 327
Qy 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
Db 328 SGNMEECEKFLRDFTENPCLRNAIOA 354

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Search completed: May 12, 2006, 02:09:35
Job time : 153.922 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2006, 02:12:04 ; Search time 19.4266 Seconds
(without alignments)
959.442 Million cell updates/sec

Title: US-10-668-936-17

Perfect score: 2131

Sequence: 1 MGLSWSPRPPLMLLVLS.....PRLPILSILPLILLQLTW 397

Scoring table: BLOSUM62

Gapex 10.0 , Gapex 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 9: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 10: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 11: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 12: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2131	100.0	397	11	US-11-253-151-33
2	577.5	27.1	444	11	US-11-253-151-33
3	574.5	27.0	464	9	US-10-745-586-112
4	505.5	23.7	468	11	US-11-253-151-35
5	490	23.0	431	11	US-11-253-151-32
6	371	17.4	273	11	US-11-253-151-8
7	364.5	17.1	258	11	US-11-253-151-9
8	132	6.2	4544	9	US-10-501-035-214
9	132	6.2	4544	11	US-11-076-427A-32
10	123	5.8	1170	11	US-11-114-962-5
11	118.5	5.6	2556	11	US-11-050-346-67
12	114.5	5.4	1433	11	US-11-114-962-1
13	110	5.2	971	8	US-10-505-928-397
14	108.5	5.1	1268	9	US-10-453-372-1144
15	108.5	5.1	1268	9	US-10-453-372-1154
16	108.5	5.1	1288	9	US-10-453-372-1146
17	108.5	5.1	1288	9	US-10-453-372-1152
18	108	5.1	1400	9	US-10-821-234-1045
19	106	5.0	2911	11	US-11-050-617-706
20	105.5	5.0	401	11	US-11-072-175-224
21	104	4.9	1193	11	US-11-022-478-8

22	103	4.8	1379	11	US-11-114-962-4	Sequence 4, Appli
23	102	4.8	999	11	US-11-113-424-36	Sequence 36, Appli
24	102	4.8	1067	11	US-11-209-137-3	Sequence 3, Appli
25	102	4.8	1067	11	US-11-054-912-3	Sequence 3, Appli
26	102	4.8	1218	9	US-10-501-035-303	Sequence 303, App
27	102	4.8	1218	11	US-11-078-735-20	Sequence 20, Appl
28	102	4.8	1218	11	US-11-050-346-65	Sequence 65, Appl
29	102	4.8	1218	11	US-11-103-077-20	Sequence 20, Appl
30	102	4.8	1218	11	US-11-072-175-155	Sequence 155, App
31	102	4.8	1218	11	US-11-022-478-4	Sequence 4, Appli
32	102	4.8	1218	11	US-11-209-137-1	Sequence 1, Appli
33	102	4.8	1218	11	US-11-054-912-1	Sequence 1, Appli
34	102	4.8	1218	11	US-11-058-066-20	Sequence 20, Appl
35	101	4.7	997	11	US-11-080-991-50	Sequence 50, Appl
36	100	4.7	728	11	US-11-022-478-11	Sequence 11, Appl
37	100	4.7	969	9	US-10-055-877-214	Sequence 214, App
38	100	4.7	1620	9	US-10-453-372-868	Sequence 868, App
39	99.5	4.7	712	11	US-11-050-857-952	Sequence 952, App
40	99.5	4.7	806	11	US-11-050-857-951	Sequence 951, App
41	99.5	4.7	970	11	US-11-050-857-950	Sequence 950, App
42	99.5	4.7	1083	11	US-11-050-857-949	Sequence 949, App
43	99.5	4.7	1292	11	US-11-050-857-948	Sequence 948, App
44	99.5	4.7	1346	11	US-11-050-857-947	Sequence 947, App
45	99.5	4.7	1419	11	US-11-114-962-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-11-253-151-33
; Sequence 33, Application US/11253151
; Publication No. US2006069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIR, MIROSLAV
; TITLE OF INVENTION: NEUROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 33
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-253-151-33

Query Match	100.0%	Score	2131	DB	11	Length	397
Best Local Similarity	100.0%	Pred. No.	1.1e-191				
Matches	397	Conservative	0	Mismatches	0	Indels	0
Qy	1	MGLSWSPRPPLMLLVLSLWPLGAGNSLATENFVNSCTOARKKCEANPACKAAQYH	60				
Db	1	MGLSWSPRPPLMLLVLSLWPLGAGNSLATENFVNSCTOARKKCEANPACKAAQYH	60				
Qy	61	LGSCTSLSRPLPLEESAMSDCLEAAEQRLNSLIDCRHRRMKHOATCLDIYTWVHPA	120				
Db	61	LGSCTSLSRPLPLEESAMSDCLEAAEQRLNSLIDCRHRRMKHOATCLDIYTWVHPA	120				
Qy	121	RSIGDYELDVSPYEDVTTSKFWONTSKLNMKPDSDCLKFMALCTLHDKCDRLRKAYG	180				
Db	121	RSIGDYELDVSPYEDVTTSKFWONTSKLNMKPDSDCLKFMALCTLHDKCDRLRKAYG	180				
Qy	181	EACSGIRCQHLCLAQIRSFPEKAAASHAGLILCCAPEDAGCGRRRTTIAPSCALPS	240				
Db	181	EACSGIRCQHLCLAQIRSFPEKAAASHAGLILCCAPEDAGCGRRRTTIAPSCALPS	240				

QY 241 VTNCNLDLRSFCRADPLCRSLMDFOHCHPMDILGTCTEQRCLRAYLGLIGTAMTN 300
DB 241 VTNCNLDLRSFCRADPLCRSLMDFOHCHPMDILGTCTEQRCLRAYLGLIGTAMTN 300
QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEATAAKRPHQLFSQDWADS 360
DB 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEATAAKRPHQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRQPRLPILSFLPILLOTLW 397
DB 361 TFSVVOQNSNPALRQPRLPILSFLPILLOTLW 397

RESULT 2

US-11-253-151-34
; Sequence 34, Application US/11253151
; Publication No. US20060069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-253-151-34

Query Match 27.1%; Score 577.5; DB 11; Length 444;
Best Local Similarity 38.8%; Pred. No. 3.7e-46;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACKAAYQHLGSCSTSSLRPLPLEESAMSADCLEAAEQLRNSLLDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLRCQLAGRDNTML-----ANKEQAALEVLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYVTVHPARSLGDYELDVSPYEDVTTSKPMKMLSKL----- 152
DB 96 KRGMKELQCLQIYWSIHLGLTEGEFYEASPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 153 -----KPDSDCLCKFAMLCITLHDKCDRLKAYGEACS-----GIRCORHLCLAQLRSPFE 202
DB 150 TDPAVTSKSNHCLDAAKACNLNDNCCKLRSSYISICNREISPTERCNRRKCHKALRQFPD 209
QY 203 KAAESHAQGLLLCPADGAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 210 RVSEYTYRMLFSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRSICRTDHLCRSR 267
QY 262 LMDFOHCHP--MDILGTCTEQRCLRAYLGLIGTAMTNPFISKVNTTVALS--CTCRG 317
DB 268 LADFHANCASRYTITSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCNCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEATA 344
DB 328 SGNMBEECEKFLRDFTEPNCLRNAIQ 354

RESULT 3

US-10-745-586-112
; Sequence 112, Application US/10745586
; Publication No. US20060063227A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.

; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6011-18X
; CURRENT APPLICATION NUMBER: US/10/745,586
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US/09/398,829
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-745-586-112

Query Match 27.0%; Score 574.5; DB 9; Length 464;
Best Local Similarity 37.9%; Pred. No. 7.5e-46;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

QY 41 CTQARKKEANPACKAAYQHLGSCSTSSLRPLPLEESAMSADCLEAAEQLRNSLLDCRC 100
DB 40 CVRANELCAAESNCSSRYRTLRCQLAGRDNTML-----ANKEQAALEVLQESPLYDCRC 95
QY 101 HRMKHQATCLDIYVTVHPARSLGDYELDVSPYEDVTTSKPMKMLSKL----- 149
DB 96 KRGMKELQCLQIYWSIHLGLTEGEFYEASPYE-PVTSR-----LSDIFRLASIFSGTG 149
QY 150 --NMLKPDSDCLCKFAMLCITLHDKCDRLKAYGEACS-----GIRCORHLCLAQLRSPFE 202
DB 150 ADPVVSAXSNHCLDAAKACNLNDNCCKLRSSYISICNREISPTERCNRRKCHKALRQFPD 209
QY 203 KAAESHAQGLLLCPADGAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
DB 210 RVSEYTYRMLFSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRGVCRTHLCRSR 267
QY 262 LMDFOHCHP--MDILGTCTEQRCLRAYLGLIGTAMTNPFISKVNTTVALS--CTCRG 317
DB 268 LADFHANCASRYTITSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCNCRG 327
QY 318 SGNLQDECEQLERSFSQNPCLVEATA 344
DB 328 SGNMBEECEKFLRDFTEPNCLRNAIQ 354

RESULT 4

US-11-253-151-35
; Sequence 35, Application US/11253151
; Publication No. US20060069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 35
; LENGTH: 468
; TYPE: PRT

	: ORGANISM: Rattus rattus	
	US-11-253-151-35	
	Query Match 23.7%; Score 505.5; DB 11; Length 469;	
	Best Local Similarity 35.6%; Pred. No. 2.2e-39;	
	Matches 127; Conservative 40; Mismatches 145; Indels 45; Gaps 13;	
Qy	10 PLMLILLVLSLWPLGAGNSLATENRFVNSTQAARKCEANPACKAAYQHILGSTSSLS 69	
Dd	11 PLLDLLMSA-----EVSGDRL-----DCVKASDQLKEQSCTKYRTLRLQCVAKGE 57	
Qy	70 RLPLEBSAMSD-CLEAAEQLRNSSLIIDCRCHRRMKHQTCLDIYTWTHPARSL-GDYE 127	
Dd	58 TNSFLTSLGLEAKDECSAMEALOKLYNRCRCKRGKKCNLCRIYWSMY--OSLQGNDL 115	
Qy	128 LDVSPEVEDTVTSKPWNLSKLNLKP-DSDL-----CLKFAMLCTLHDKCDD 174	
Dd	116 LEDSPYE-----PVNSRLSIDFRAPVFISDVQQVEHIHSKGNCLDAKACNLDDTCK 169	
Qy	175 LRKAYGEAC----SGIRCQRHLCLAQLRSFFFEKAESHAOGLLLCPCAPEDAGCGERRRN 230	
Dd	170 YRSAYITPCTTSMNEVCNRKRCHKALROFDKVPAKHSYGMLFCSC--RDIACTERRRQ 227	
Qy	231 TIAPSCALPS-VTPNCILDLSRCDPLCRSRLMDFOPTHCPWD-ILGTCAEQ-SRCLR 287	
Dd	228 TIIVPCSYEERPNCLSLQDSCKTYICRSRLADFTTCQPESRSVSNCKENTADCLL 287	
Qy	288 AYLGLIGTMTNFISKVTNTVALSCTCRSGNLODECQLERSFSQNPLVEATAA 344	
Dd	288 AYSGLIGTWTNPYNVDSSLVSUAVPWCDSCNSGNDLEDCLKFLNFKDNTCLKNALQA 344	
	RESULT 5	
	US-11-253-151-32	
	; Sequence 32, Application US/11253151	
	; Publication No. US20060069242AI	
	; GENERAL INFORMATION:	
	; APPLICANT: MASURE, STEFAN L.J.	
	; APPLICANT: CIK, MIROSLAV	
	; APPLICANT: HOEFNAGEL, EVERT W.	
	; TITLE OF INVENTION: NEUTROTROPIC FACTOR RECEPTOR	
	; FILE REFERENCE: JAB-1512	
	; CURRENT APPLICATION NUMBER: US/11/253,151	
	; PRIOR FILING DATE: 2005-10-18	
	; PRIOR FILING DATE: PCT/EP00/04918	
	; PRIOR FILING DATE: 2000-05-26	
	; PRIOR APPLICATION NUMBER: GB 9915200.1	
	; PRIOR FILING DATE: 1999-06-29	
	; NUMBER OF SEQ ID NOS: 48	
	; SOFTWARE: PatentIn Ver. 3.2	
	; SEQ ID NO 32	
	; LENGTH: 431	
	; TYPE: PRRT	
	; ORGANISM: Gallus gallus	
	US-11-253-151-32	
	Query Match 23.0%; Score 490; DB 11; Length 431;	
	Best Local Similarity 32.8%; Pred. No. 5.6e-38;	
	Matches 120; Conservative 50; Mismatches 158; Indels 38; Gaps 12;	
Qy	41 CTOARKECANPACKAAYQHLSCTSLSRLPBLESAMSDCLAEAEOLRNSSLIDCRC 100	
Dd	26 CLQAGESBTDPICSSKFTRLRQCIAG-NGANKLGPDAXN-QCRSVTTALLSSQLYGCCK 83	
Qy	101 HRRMKHQATCLDIYTWTHPARSLGDYELDSPYEDTVTSKPWNLSKLNLKPDS--- 157	
Dd	84 KRGMKKKHCLSVMYSHIHTLMEGMNVLESSEPYEPIRG-----FDYVLASITAGESEV 139	
Qy	158 ----LCLKPAMLCTLHDKDLRKAYGEACSGIR-----CORHLCLAQLRSFPFEKAAE 206	
Dd	140 TVNQNRCLDRAKANDEMCOURLTEVTSFC--IRRLEARDTNCRSKCHKALKKFDVRPP 197	
Qy	207 SHAQGLLLCPCAPEDAGCGERRRNTTIAPSALPS-VTPNCLDLRSFCRADPLCRSLDMDF 265	

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; ORGANISM: Rattus rattus
US-11-253-151-35

Query Match      23.7%; Score 505.5; DB 11; Length 468;
Best Local Similarity 35.6%; Pred. No. 2.2e-39;
Matches 127; Conservative 40; Mismatches 145; Indels 45; Gaps 13;

Qy 10 PLMLILLVLSLWPLGAGNSLATERNFVNSTCAARKCEANPACKAAYQHILGSTSSLS 69
Db 11 PLLDLLMSA-----EVSGDRL-----DCVKASDQLKEQSCTKYRTLRCQCVAKGE 57

Qy 70 RPLPLESAMSAD-CLEAAEQLRNSSLIIDCRCHRRMKHQATCLDIYTWTHPARSL-GDYE 127
Db 58 TNFSLTSLGLEAKDECSAMEALKOKLYNCRCKRGKKCKNLRIYWSMY--OSLOQNGL 115

Qy 128 LDVSPEVEDTVTSKPWNLSKLNNLP-DSDLL-----CLKFAMLCTLHDKCDR 174
Db 116 LEDSPYE-----PVNSRLSIDIFRAVPFFISDFVQQVEHISKGNCLDAKACNLDDTCX 169

Qy 175 LRKAYGEAC----SGIRCQRHLCLAQLRSFFEKAESHAOGLLCPCAPEDAGCGERRRN 230
Db 170 YRSAYITPCTTSMNEVCNRKCHKALROFFDKVPKHSYGMLFCSC--RDIACTERRRQ 227

Qy 231 TIAPSCALPS-VTPNCILDLSFRADPLCSRLLMDFOETHCPWD-ILGTCAEQ-SRCLR 287
Db 228 TIVPVCSYEERPNCLSLQDSCKTYICRSRLADFTTNCOPESRSVSNCKENYADCLL 287

Qy 288 AYLGIGTGATMPNFISKNTVALSCTCRGSNLODECQEOLERSFSONPCLVEATAA 344
Db 288 AYSGLIGTVMTPNYDVSSLSLVAPWCDCSNSNDLEDCLKFLNFDKNTCLKNALQA 344

RESULT 5
US-11-253-151-32
; Sequence 32, Application US/11253151
; Publication No. US20060069242AI
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUTROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR FILING DATE: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 32
; LENGTH: 431
; TYPE: PRP
; ORGANISM: Gallus gallus
US-11-253-151-32

Query Match      23.0%; Score 490; DB 11; Length 431;
Best Local Similarity 32.8%; Pred. No. 5.6e-38;
Matches 120; Conservative 50; Mismatches 158; Indels 38; Gaps 12;

Qy 41 CTOARKECANPACKAAYQHLSCTSLSRPIPLEBSAMSDCLAEAEQLRNSSIIDCRC 100
Db 26 CLQAGESBTDPICSSKFRTLRQCIAG-NGANKJGDAXN-QCRSTVTALLSSQLYGCKC 83

Qy 101 HRRMKHQATCLDIYTWTHPARSLGDYELDVSYPEDTVTSKPWNLSKLNNLPKDPD--- 157
Db 84 KRGMKKEKHCLSIVSYHHHTLBEGMNVLESSEPYEPIRG-----PDYVLASITAGESEV 139

Qy 158 ----LCLKPAFMLCTLHDCKDLRKAYGEACSGIR-----CORHLCLAQLRSFPFEKAAE 206
Db 140 TVNQNRCLDAAKCNVDQMQRULTEVVSFC--IRRRLRADTCNRSKCHKALKKFFDRVPP 197

Qy 207 SHAQGILLCCPADGACGERRRNTIAPSALPS-VTPNCILDLSFRADPLCSRLLMDF 265
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; TITLE OF INVENTION: NEUROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Rattus rattus
; ORGANISM: Rattus rattus
US-11-253-151-9

Query Match      17.1%; Score 364.5; DB 11; Length 258;
Best Local Similarity 35.1%; Pred. No. 1.7e-26;
Matches 86; Conservative 26; Mismatches 102; Indels 31; Gaps 7;

QY 142 WKNLSKLNMLKPDSDLCLKFAMLTCLHDKDRLKAYGEACSGI-----RCQRHLCL 194
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 20 WSLGCGQSGASSTEGNRCVVEAAEACTADEQCQQLRSEYVAQCLGRAGWPGSCVRSRCR 79

QY 195 AOLRSFPEKAASHQAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS---VTPNCLDLRSF 251
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 RALRRFPAGPPALTHALLFCGC---EGPACAEERRQTAPACAFSGPOLAPSCCLKPLDR 137

QY 252 CRADPLCRSLMDPQTHCHPMILGT---CATEQS--RLRAYLGLIGTAMTNFISKVNT 307
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 CERSRRCPRLPAFQASCAPAP---GSRDGPCEGGPRCLRAYAGLVGTVTNYLDNVA 195

QY 308 TVALSTCRSGNLODEQLERSPSQNCPLVEAIAAKMRFHRLQSFQDWDSTFVVOQ 367
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 196 RVAPWCGCEASGNRREECEAFRLKLFTRNPLDGAIOA-----FDSQSPSVLQ 242

QY 368 QNSNP 372
   ||
DB 243 DOWNP 247

RESULT 8
US-10-501-035-214
; Sequence 214, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-501-035-214

Query Match      6.2%; Score 132; DB 9; Length 4544;
Best Local Similarity 20.2%; Pred. No. 0.0033;
Matches 78; Conservative 35; Mismatches 142; Indels 132; Gaps 20;

QY 62 GSCTSSLSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRM-----KHOATCL 111
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2615 GTCIGNSSR-----CNQFVDCEDASDEM-NCSATDCSSYFRLGVKGVLFQPCERTSLCY 2667

QY 112 DIYTVHPARSLGDYELDVSPYEDVTTSKPKWNLSKLNMLKPDSDLCLKFAMLTCLHDK 171
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2668 APSWVCDGANDCGD-----YSDERDCPGVKRPRCPNLNYFACPSGRCPMSWTCDKEDD 2720

QY 172 CDRLRKAYGE-----ACS--GIRCQRHLCLAQ-----LRSFPEKAASHQAQ-- 211
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2721 CE-----HGEDETHCNKFCSEAQFECQNRHCLSKQWLCDGSDDCDGDGSDDEAA--HCEGKT 2773

QY 212 ----LLLCF-----CAPE-----DAGCGERRNTIAPSCALPSVTPN-----CLDL 248
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2774 CGPSSFCFGTHVCVPERWLCDGDKDCADGADESIAAGCLYNSTCDDREFMCONRQCIPK 2833

QY 249 RSFCRAD-----PLC-----RSRLMDFQTHCHPMILGT- 277
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2834 HFVCDHDRDCADGSDSPCEPYTCGPSEFRFCANGRCILSSRQWECDEGNDCHDQSDAPK 2893

QY 278 ---CATEQSRCLRAYLGLIGTAMTNFISKVNTTVALSCTCRSGNLODEC---EQLETSF 332
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2894 NPHCTSPBHKC-----NASSQFLCSSGRCAEALLCNG-----QDDCGSSDERGC 2939

QY 333 SQNPCLVEAIAAKMRFHRLQSFQDWD 359
   ||
DB 2940 HINECLSRKLSG-----CSQDCED 2958

```

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DB 2668 APSWVCDGANDCGD-----YSDERDCPGVKRPRCPNLNYFACPSGRCPMSWTCDKEDD 2720

QY 172 CDRLRKAYGE-----ACS--GIRCQRHLCLAQ-----LRSFPEKAASHQAQ-- 211
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2721 CE-----HGEDETHCNKFCSEAQFECQNRHCLSKQWLCDGSDDCDGDGSDDEAA--HCEGKT 2773

QY 212 ----LLLCF-----CAPE-----DAGCGERRNTIAPSCALPSVTPN-----CLDL 248
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2774 CGPSSFCFGTHVCVPERWLCDGDKDCADGADESIAAGCLYNSTCDDREFMCONRQCIPK 2833

QY 249 RSFCRAD-----PLC-----RSRLMDFQTHCHPMILGT- 277
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2834 HFVCDHDRDCADGSDSPCEPYTCGPSEFRFCANGRCILSSRQWECDEGNDCHDQSDAPK 2893

QY 278 ---CATEQSRCLRAYLGLIGTAMTNFISKVNTTVALSCTCRSGNLODEC---EQLETSF 332
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2894 NPHCTSPBHKC-----NASSQFLCSSGRCAEALLCNG-----QDDCGSSDERGC 2939

QY 333 SQNPCLVEAIAAKMRFHRLQSFQDWD 359
   ||
DB 2940 HINECLSRKLSG-----CSQDCED 2958

RESULT 9
US-11-076-427A-32
; Sequence 32, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENO
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-076-427A-32

Query Match      6.2%; Score 132; DB 11; Length 4544;
Best Local Similarity 20.2%; Pred. No. 0.0033;
Matches 78; Conservative 35; Mismatches 142; Indels 132; Gaps 20;

QY 62 GSCTSSLSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRM-----KHOATCL 111
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2615 GTCIGNSSR-----CNQFVDCEDASDEM-NCSATDCSSYFRLGVKGVLFQPCERTSLCY 2667

QY 112 DIYTVHPARSLGDYELDVSPYEDVTTSKPKWNLSKLNMLKPDSDLCLKFAMLTCLHDK 171
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2668 APSWVCDGANDCGD-----YSDERDCPGVKRPRCPNLNYFACPSGRCPMSWTCDKEDD 2720

QY 172 CDRLRKAYGE-----ACS--GIRCQRHLCLAQ-----LRSFPEKAASHQAQ-- 211
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2721 CE-----HGEDETHCNKFCSEAQFECQNRHCLSKQWLCDGSDDCDGDGSDDEAA--HCEGKT 2773

QY 212 ----LLLCF-----CAPE-----DAGCGERRNTIAPSCALPSVTPN-----CLDL 248
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2774 CGPSSFCFGTHVCVPERWLCDGDKDCADGADESIAAGCLYNSTCDDREFMCONRQCIPK 2833

QY 249 RSFCRAD-----PLC-----RSRLMDFQTHCHPMILGT- 277
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2834 HFVCDHDRDCADGSDSPCEPYTCGPSEFRFCANGRCILSSRQWECDEGNDCHDQSDAPK 2893

QY 278 ---CATEQSRCLRAYLGLIGTAMTNFISKVNTTVALSCTCRSGNLODEC---EQLETSF 332
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2894 NPHCTSPBHKC-----NASSQFLCSSGRCAEALLCNG-----QDDCGSSDERGC 2939

QY 333 SQNPCLVEAIAAKMRFHRLQSFQDWD 359
   ||

```



```
; SEQ ID NO 1
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-114-962-1

Query Match      5.4%; Score 114.5; DB 11; Length 1433;
Best Local Similarity 19.9%; Pred. No. 0.035;
Matches 85; Conservative 40; Mismatches 132; Indels 171; Gaps 26;

QY 39 NSCTQARKKEANPA-----CKAAYQHLAGSCTSSLRPLPLESAMSAD-CLEAARQLRN 92
DB 379 NPCNEG-SNCDTPVNGKAICTCPRGVGPACSQ-----DVDESCALGANPCEHAGKCLNT 432
QY 93 SSIIIDRC-----HRRMKHQATCLDIYVTHVPARSGLGDYELDVSP-YE 134
DB 433 LGSFEQCCLQGYTGPRCEIDVNECISNPQNDAATCLD-----QIGEFQICMPGYE 483
QY 135 -----DVTGSKPMKN--LKLN-----MLKPDSDLCLK----- 161
DB 484 GVTCEINTDECASSPCLHNGRCVDKINEFLCQPKGFSGLHCQYDVDECASTPCKNGAKC 543
QY 162 -----FAMLC-----LH-----DKCDRLRKAYGACSGIR-----CQ-----RHLCIAQ 196
DB 544 LDGPNTYTCVCTEGYTGTHCEVDIDECDDPDCHIGLCKDGVATFTCLCQPGYTGHCETN 603
QY 197 LRSEFFKAESHAQGLLLCPCAPEDAGCGERRNTIAPSCALPSVTPNCLDLRSFCRADP 256
DB 604 IN-----ECHSQ-----PC--RHGGTCQDRDNYLYLCLKGTTGPNCEINLDDCASNP 649
QY 257 -----LCRSRLMDFTCHP-----MDIL-----GTC-----ATEQSRCLRAYL 290
DB 650 CDSGTCLDKIDGECACEPEGYTGSMCNVNIDEAGSPCHNGGTCEDGIAGFTCRCEGY- 708
QY 291 GLIGTAMTPNFISKVNTVALSC---TCRGSNG-----LQDECEQLER 330
DB 709 -----HDPTCLSEVNECSNPCHGACRDGLNGKDCAPGWSGTNCDINNNECE- 758
QY 331 SFSQNPCL 338
DB 759 ---SNPCV 763

RESULT 13
US-10-505-928-397
; Sequence 397, Application US/10505928
; Publication No. US2006089532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 397
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-397

Query Match      5.2%; Score 110; DB 8; Length 971;
Best Local Similarity 19.7%; Pred. No. 0.057;
Matches 100; Conservative 56; Mismatches 168; Indels 182; Gaps 26;

QY 22 WLPPLGAGN-SLATENRFVNSCTQARKKEANPACKAAYQH-LGSCTS----- 66
DB 99 WVGLGCCELAIALECR--QACKQSSKNDISKVCKREYNALFSCISRNEMGVCCSYAG 156
QY 67 -----SLSRPLPLEESAMSADCLEAAEQ-----RN--SSLID 97
```

```
DB 157 HHTNCREYQCAIFRTDSSPGPSQIKAVENYCASISPQLIHCVNNYTSQYPMENPTDLSLYC 216
QY 98 C-----RCHRMKHQATCLDI-----YW-----T 116
DB 217 CDRAEDHACQNAACKRIILMSKKTEMEIVDGLIEGCKTQPLPODPLWQCFLLESSQSVHPGVT 276
QY 117 VHPARSLG-DYELDVSPVEDTIVT-----SKPMKKNLSKLNMLKPDSDLCL-1KFAML 165
DB 277 VHPFPSTGLDGAKLHCCSKANTSTCRELCTKLYNSWGNQTSQWQEFDFCEYNPVEVSNL 336
QY 166 CTLHD-----KCDRL-----RKAYGEACSGI----- 186
DB 337 TCLADVREPQQLGCRNLATYCTFNFNRRPTTELFSCNAQSDQCAMNDMLKWEKSIKMPFIN 396
QY 187 -----RCORHLCIAQLRSFPEKAESHAQGLLLC--PCAPEDAGCGERR-NTIA 233
DB 397 IPVLDIKKQCPQPMWKAIACSLQIKPCKSKRSRGIICKSDCVILKKCGDQNKFPEDHTAE 456
QY 234 PSCALPSVT---PNCCLDLRSFCRADPPLCRSRLMDPQTH-CHPMDILGTCATEQSR----- 284
DB 457 SICELLSPTDDLKNCIPLDITYLR--PSTLGNIVEVTHPCNPENPCANELCEVNRKGCPS 514
QY 285 ---CLRAYLGLIGTAM--TPNPFISKVNTVALS-----CTCRSGNLQDECEQL 328
DB 515 GDPCL-PYFCVQCKLGEASDFIVRQGTLIQVPSSAGEVGYKICSC-GQSGLLNCMEM 572
QY 329 ERSFSQNPCLVEAIAAKMRFHRLQLESQD 356
DB 573 HCIDLQKSCIV--GGRKRSHGTSPSID 597

RESULT 14
US-10-453-372-1144
; Sequence 1144, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Aleobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1144
; LENGTH: 1268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1144

Query Match      5.1%; Score 108.5; DB 9; Length 1268;
Best Local Similarity 21.1%; Pred. No. 0.11;
Matches 85; Conservative 34; Mismatches 159; Indels 125; Gaps 21;
```

```

Qy 25 LGAGNSLATENRFVNSCTQARK--KCEAN-----PACKAAYQHLGSCSTSSLSRPLPLE-- 75
Db 272 LGGSCVDLVGNVTCLCAEPFKGLRCETGDHPVPDACLAPCHNGGTCVDADQGVVCECP 331
Qy 76 ESAMSDACLEAAEQLRNSSLIDCHRRMKHQATCLDIYWTVHPARSLGDYELDVSPYED 135
Db 332 EGFMLDCRERVDP-----DCEC-----RNGRCGLGANTTLCQC-PLGFFGL-LCBFE- 377
Qy 136 TVTSKPMKMLSKLNMKLPDSDCLCKF--AMLCTLH-----DKC 172
Db 378 -ITAMPQNMNTQ-----CPDGGYCMHGSSYLCVCHTDHNASHSLSLPSDCSDPCFNGGSC 431
Qy 173 DRLRKAYGEAC-----SGIRCQ-----HLCLA-----QLRSFPEKAASHAQ----- 210
Db 432 DAHDDSYTCBPRGFHGKHKCEKARPHLCSSGPCRNGGTCKEAGGEYHCSCPFRFTGRHCE 491
Qy 211 -----GULLCPCAPEDAGCGERRNTTAPS-CALPSVTTPNCLD 247
Db 492 IGKPDSCASGPNCHNGGTCFHYIGKYKDCPPGFSG-----RHCEIAPSPC----- 536
Qy 248 LRSFCRADPLCRSLMDFTQTHCPMDILGTCAE-----QSRCLRAYLGLIGTAMTNPFI 302
Db 537 FRSPCVNGGTCEDRDTDFCHCQAGYMGRCQAEVDCGPPPEVKHATLRFNGTGLGAVAL 596
Qy 303 SKYNTTVALS-----CTCRSGNLQDECEQLERSFSQNPCL 338
Db 597 YACDRGYSLAPSRIQVCPHGVSPPQCLIDECRSQ-PCL 638

```

Search completed: May 12, 2006, 02:16:16
Job time : 20.4266 secs

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RESULT 15
US-10-453-372-1154
; Sequence 1154, Application US/10453372
; Publication No. US2006003233A1
; GENERAL INFORMATION:
; APPLICANT: Alisobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 1154
; LENGTH: 1268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1154

```

Query Match 5.1%; Score 108.5; DB 9; Length 1268;
Best Local Similarity 21.1%; Pred. No. 0.11;
Matches 85; Conservative 34; Mismatches 159; Indels 125; Gaps 21;

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:04:54 ; Search time 25.596 Seconds
(without alignments)
1503.623 Million cell updates/sec

Title: US-10-668-936-21

Perfect score: 2190
Sequence: 1 MVRPLNRPPLPPVVMMLLL.....PWVPSLFSCTPLPLILLSLW 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1646.5	75.2	397	2 JE0082	GPI-linked recepto
2	147	6.7	2703	1 A24420	notch protein - fr
3	133.5	6.1	3084	1 MMSB2	laminin alpha-1 ch
4	124	5.7	1700	2 S08167	Balbani ring 3 pr
5	123.5	5.6	2195	2 T34264	hypothetical prote
6	123.5	5.6	2871	2 A55567	fibrillin I - bovi
7	123.5	5.6	3002	2 A47221	fibrillin 1 precur
8	120	5.5	1964	2 T09059	notch4 - mouse
9	117.5	5.4	2704	2 S09118	G surface protein
10	116	5.3	3635	2 T10053	laminin alpha 5 ch
11	115	5.3	2531	2 A46019	notch-1 protein -
12	115	5.3	5376	2 T42215	zonadhesin - mouse
13	114.5	5.2	1106	2 T44598	hypothetical prote
14	114.5	5.2	2871	2 A55624	fibrillin-1 precur
15	114	5.2	1034	2 JC5598	mucin - rat
16	114	5.2	2531	2 S18188	notch protein homo
17	112.5	5.1	2555	2 A40043	notch protein homo
18	112.5	5.1	4543	1 A53102	alpha-2-macroglobu
19	111.5	5.1	1106	2 T13938	gene shuttle craft
20	111.5	5.1	1609	1 MMHUB2	laminin gamma-1 ch
21	110	5.0	2321	2 S78549	notch3 protein - h
22	110	5.0	4544	1 S02392	alpha-2-macroglobu
23	109.5	5.0	949	2 T24294	hypothetical prote
24	109	5.0	2139	2 A35672	crumbs protein - f-
25	108.5	5.0	4545	1 S25111	alpha-2-macroglobu
26	108	4.9	2718	2 A23475	G surface protein
27	106	4.8	473	2 A56175	adhesive plaque pr
28	106	4.8	2918	2 A54105	fibrillin-2 precur
29	105	4.8	593	2 S45281	coagulation factor

30	105	4.8	1607	1 MMSB2	laminin gamma-1 ch
31	105	4.8	1959	1 AGRT	agrin - rat
32	105	4.8	2907	2 A57278	fibrillin-2 precur
33	105	4.8	3075	2 S14458	laminin alpha-1 ch
34	104	4.7	593	1 GHU	granulin precursor
35	104	4.7	1203	2 A49175	Notch B protein -
36	104	4.7	1639	1 MMFFB2	laminin gamma-1 ch
37	104	4.7	2352	2 T30201	Notch homolog prot
38	104	4.7	2471	2 A49128	cell-fate determin
39	103.5	4.7	384	2 S25771	gas1 protein - mou
40	103	4.7	2150	2 T32497	hypothetical prote
41	102.5	4.7	2318	2 S45306	notch 3 protein -
42	101.5	4.6	1661	2 T31330	head-activator bin
43	101	4.6	1077	2 T41146	probable cysteine-
44	100.5	4.6	1984	2 T13171	probable vitelloge
45	100	4.6	1513	2 T23681	hypothetical prote

ALIGNMENTS

RESULT 1

JE0082

GPI-linked receptor precursor - mouse

N;Alternate names: GFRalpha-3

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C;Accession: JE0082

R;Noto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.

Biochem. Biophys. Res. Commun. 244, 849-853, 1998

A;Title: Molecular cloning and expression analysis of GFRalpha-3, a novel cDNA related to

A;Reference number: JE0082; MUID:98205811; PMID:9535755

A;Accession: JE0082

A;Molecule type: mRNA

A;Residues: 1-397 <NOM>

A;Cross-references: UNIPROT:O35118; UNIPARC:UPI000002321A; DBJ:AB008833; NID:92627159;

C;Comment: This protein plays a distinct role in cell survival and differentiation.

C;Superfamily: Mus musculus GPI-linked receptor

C;Keywords: glycoprotein

F;1-25/Domain: signal sequence #status predicted <SIG>

F;380-397/Region: hydrophobic

F;92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	75.2%	Score	1646.5	DB 2	Length	397
Best Local Similarity	77.8%	Pred. No.	1.5e-122			
Matches	305	Conservative	30	Mismatches	56	Indels 1; Gaps 1;
Qy	9	PLPPVLMILLPLPPPLPLAAGDPLPTESLMNSCLQARRKQADPTCSAAVHLLDSCT	68			
Db	7	PRPP-LIMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAVQHLGSGCT	65			
Qy	69	SSISTPLPSEPSVPADCLAAQOLNSSLIGWCCHRRMKNVACLIDIVTVHRAESIGN	128			
Db	66	SSLSRPLPLESANSADCLAAEQRLNSSLIDCRCHRRMKHQATCLDIIYTVHAPRSLGD	125			
Qy	129	YELDVSPYEDTVTSKFWKMLSKLMLKPDSDLCLFAMLTCLNDKCDRLRKAYGEACSG	188			
Db	126	YELDVSPYEDTVTSKFWKMLSKLMLKPDSDLCLFAMLTCLNDKCDRLRKAYGEACSG	185			
Qy	189	PHQHVCLRLQLTFEKAAPHAQGLLLCPAPNDRGCGGERRRNTAPNCALPPVAPNC	248			
Db	186	IRCQRHLCAQLASFFEKAAESHAQGLLLCPAPNDRGCGGERRRNTAPNCALPPVAPNC	245			
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A;Cross-references: UNIPARC:UPI0000173CAA; UNIPARC:UPI0000173CAE
R;Deutmann, R.; Huber, J.; Schmetz, K.A.; Oberbauer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-termini in laminin alpha-1 chain.
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submitted to the EMBL Data Library, November 1995
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RESULT 6

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C:Accession: A55567
R:Ritstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.
Genomics 23, 480-485, 1994
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Db 2278 PGYQRRPDGEGCVDENECQTKPGICENGRCCLNTRGSYTCECN---DGFTA----- 2324
QY 153 NMLKPDSDLCLK----FAMLTCLNDKC-----DLRKAYGEACS-----GPHCQRHVCL 197
Db 2325 ---SPNQDECLNDRREGYCFTEVLQNMCIQSGSNRPVTKSECCDGGRGWGPHE--ICP 2379
QY 198 ROLLTFEKAAPHAQGLL-----LC---PCAPNDRGCGERRRNTIAPNCA 240
Db 2380 FGQTVAFKLC-PHGRGFWNGADIDECKVIHDCVNGECV-NDRG----SYHCICKGY 2433
QY 241 LPFVAPN-CLELRRLCFSDP-----LCRSLRVDFQTHCHPMDI-----LGTCAE 284
Db 2434 TPDITGTACVDLINE-CNOAPKPCNFICKNTGEGYQCSCKPGYILOEDGRCSDLDCAATK 2492
QY 285 QSRCLRAYLGLIGT---AMTNFVSN-----VNTSVALSCTC 318
Db 2493 QHNCFLCVNTIGTSFTCKCPGFTQHTTACIDNNECTSDINLCGSKGICQNTPGSFTCEC 2552
QY 319 R-----GSGNLQEBCEML-----EGFFSH-----NPCL 341
Db 2553 QRGFSLDPTGASCDVDCEGHNRCQHGQNIIGGYRCSCPQGYLQHYQWNCVDENECL 2612
QY 342 TEAIAAKMRFHSQIFS 357
Db 2613 SAHICGGASCHNTLGS 2628

RESULT 7

A47221
fibrillin 1 precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 31-Dec-2004
C:Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198
R:Corson, G.M.; Chaberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
Genomics 17, 476-484, 1993
A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure
A:Reference number: A47221; MUID:94010947; PMID:7691719
A:Accession: A47221
A:Molecule type: mRNA
A:Residues: 1-337, T', 339-1029 <COR>
A:Cross-references: UNIPROT:P35555; UNIPROT:Q15972; UNIPROT:Q9NP01; UNIPARC:UPI000017651
R:Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan, T.; Bona
Hum. Mol. Genet. 2, 961-968, 1993

A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene F
A;Reference number: 154355; MUID:93372860; PMID:8364578
A;Accession: I54355
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 132-3002 <PBR>
A;Cross-references: UNIPARC:UPI0000055AD1; GB:L13923; NID:9306745; PIDN:AB02036.1; PID:
R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
Nature 352, 334-337, 1991
A;Title: Partial sequence of a candidate gene for the Marfan syndrome.
A;Reference number: S17064; MUID:91304568; PMID:1852207
A;Accession: S17064
A;Molecule type: mRNA
A;Residues: 1030-3002 <MAS>
A;Cross-references: UNIPARC:UPI0000176517; EMBL:X63556
R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
Science 259, 680-683, 1993
A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
A;Reference number: I59574; MUID:93157831; PMID:8430317
A;Accession: I59574
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 2217-2288, 'I', 2290-2325 <RES>
A;Cross-references: UNIPARC:UPI000006FPF6; GB:S54426; NID:9264860; PIDN:AB25244.1; PID:
R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different
A;Reference number: S17062; MUID:91304567; PMID:1852206
A;Accession: S17062
A;Molecule type: mRNA
A;Residues: 'VLVTWVFILSNKWL', 944-1444 <LEE1>
A;Cross-references: UNIPARC:UPI0000072A79; EMBL:X62008; NID:G31398; PIDN:CAB56534.1; PID:
A;Accession: S62111
A;Molecule type: protein
A;Residues: 1166-1176, 'Y', 1178-1180, 'D', 1182-1185 <LEE2>
A;Cross-references: UNIPARC:UPI0000176518
R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
A;Title: Connective tissue microfibrils. Isolation and characterization of three large p
A;Reference number: A34198; MUID:90078246; PMID:2512293
A;Accession: A34198
A;Molecule type: protein
A;Residues: 565-575/1890-1892, 'I', 1894-1900 <MAD>
A;Cross-references: UNIPARC:UPI0000176519; UNIPARC:UPI000017651A
C;Comment: Fibrillin is a major component of elastin-associated microfibrils.
C;Genetics:
A;Gene: GDB:FBN1
A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700
A;Map position: 15q21.1-15q21.1
A;Introns: 2236/1; 2258/1; 2297/1
C;Superfamily: EGF homology
C;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
F;1302/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted
F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MAD>
F;1332-1367/Domain: EGF homology <EGF>
F;1457-1492/Domain: EGF homology <EGF2>
F;2262-2295/Domain: EGF homology <EGF1>

Query Match 5.68; Score 123.5; DB 2; Length 3002;
Best Local Similarity 19.34; Pred. No. 0.23;
Matches 84; Conservative 46; Mismatches 131; Indels 175; Gaps 25;

QY 48 RRKQADPTCSAAVYHLDSTSSITPLPSEPSVPADCLEAAQQLRNSSLIG---CMC- 103
DB 2373 RRKCKDECEEGKH-----DCTEKQNECKN--LIGTYMCIG 2408

QY 104 --HRRMKNQVACLD-----IYTWVTHARSIGNYELDVSPYEDVTTSKPKWMLSKL 152
DB 2409 PGYQRPDGGGVDENEBCQTKPGICENGRCINRGSVTCEN---DGFTA----- 2455

QY 153 NMLKPDSDCLCK-----FAMLCITLNDKC-----DLRLKAYGEAS-----GPHCQRHVCL 197
DB 2456 ---SPNQDECLNREGYCFTEVLQNMCMQIGSSNRNPVTKSECCCDGGRGWGPCHCE--ICP 2510

QY 198 RQLLTFFEKAAEPHAQGLL-----LC-----PCAPNDRGCGERRRNTIAFNCA 240
DB 2511 FQGTVAFFKLC- PHERGFWTNGADIDBECKVIHVDVCRNGECV-NDRG---SYHCICKTGY 2564

QY 241 LPV-APNCLLELRRLCFSDP-----LCRSLVDFQTHCHPMDI-----LGTGATE 284
DB 2565 TPDITGTCVDLNE-CNQAPKPCNFCKNTEGYSQCSKPYLQEDGRSKOLDDECATK 2623

QY 285 QSRCLRAYLGLIG--TAMTPNFVSN-----VNTSVALSCTC 318
DB 2624 QHNCQFLCVNTIGFTCKCPPGFTQHTSCIDNNECTSDINLCGSKGICQNTPGSPFCBC 2683

QY 319 R-----GSGNLOEBCML-----EGFFSH-----NPCL 341
DB 2684 QRGFSLDQTSCEDECEGNHRCQHGQNIIGYRCSCPQYLYHQWQNCVDENECL 2743

QY 342 TEAIAAKMRPHSOLF 357
DB 2744 SAHICGGASCHNTLGS 2759

RESULT 8
T09059
notch4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.;
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09059
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:92564945;
C;Genetics:
A;Gene: notch4
A;Map position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 619/3; 1729/1; 1761/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology <EGF>

Query Match 5.58; Score 120; DB 2; Length 1964;
Best Local Similarity 22.86; Pred. No. 0.28;
Matches 81; Conservative 30; Mismatches 135; Indels 112; Gaps 22;

QY 51 CQADPTCSAAVYHLDSTSSITPLPSEPSVPADCLEAAQQLRNSSLIGCMC----- 103
DB 417 CQPGYSGSTCHQDLDCQWQAQGPSP-----CEHGSCINTPGSFNCLCLPGVTGS 467

QY 104 -----HRRMKNQ-----VACLDIYTWVTHARSIG-----NYELDVSPYEDVTTSKPKWML 149
DB 468 RCEADHNECLSQPCPGSTCLDLATFHLCLCPGLEGRLECEVEV-----NECTSNPCLNQA 523

QY 150 SKLNLKPDSDCLCK--FAMLCITLN-DKDLRLKAYGEAC-----SGPHC 191
DB 524 ACHDLLNGFQCLCLPGFTGARCEKMDCSSTPCANGRCRDQPGAFYCECLPGFEGPHC 583

QY 192 QRHV-----CLRQLLTFFEKAAEPHAQGLL-----LCP---CAPNDRGGGERR 231
DB 584 EKEVDECLSDPCPVGASCLDLPGAFP-CLCRPGFTQQLCEVPLCTPNMCPGQCGOQOE 642

QY 232 RNTIAPNCALPPVAPNCLLEL-----RRLCFSD-----PLCRSLVD-FQTHC- 272
DB 643 R---AP-CLCPDGSPCVPAEDNCPCHGHCQSLCVCDEGWTGPCETELGCISTPCA 698

QY 273 HPMIDLGTGATES-----RCLRAYLGI-----IGTAMTFNVSNVTSV---ALSTC 318
DB 699 HG-----GTCHPOPSGYNCTCPAGYMLTCSSEVTAHSGCLNGGSGSRPEGSCTC 752

RESULT 9
S09118
G surface protein 168 - Paramesicium primaurelia
C;Species: Paramesicium primaurelia
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S09118
R;Prat, A.
J. Mol. Biol. 211, 521-535, 1990
A;Title: Conserved sequences flank variable tandem repeats in two alleles of the G surface
A;Reference number: S09118; MUID:90172419; PMID:2308165
A;Accession: S09118
A;Molecule type: DNA
A;Residues: 1-2704 <PRA>
A;Cross-references: UNIPROT:P17053; UNIPARC:UPI000012AE23; EMBL:X52133; NID:g10049; PIDN:
C;Genetic code: SGCS
C;Superfamily: G surface protein

Query Match 5.4%; Score 117.5; DB 2; Length 2704;
Best Local Similarity 19.5%; Pred. No. 0.61;
Matches 79; Conservative 32; Mismatches 136; Indels 159; Gaps 17;

QY 45 LQARRKQADPTCSAAHHLDSTSSISPLPSEPSV-----PADCLEAAQ 92
Db LACRNATCADAPDTAY---DSDECLAYPTPSETCTVYKGAQCVCKSANC----- 848

QY 93 LRNSSLIGCMCHRMKNQVACLDIYTVHRARSLGNYELDVSPYEDTVTSKPKMNL SKL 152
Db --SDYMTSAQCHTKLTNLNTANDCKWIDRCYALSSFA-----TGAC 888

QY 153 NMLKPSDCLCKFAMLCNTLNDCKRLKAYGEACSPHCORHVCLRLQLLTFPEKAAPHA 212
Db TTFKGNKTMCEGYRAGCT-----NTVG-AASSASCTLDCTLKT-----G 926

QY 213 QGLLCPCPNDRGCCERRNT---IAPNCA-LPPVAPNCLL-----LRLRCFSPLCKR 262
Db SGLTFADQCQALDSTCSVKDGTGCVIOSTCAGYGTATNCFRSSASGTAGYCAMNTNCQ 986

QY 263 S-----RLVDFOFHCHPM-----DIIG 279
Db SVTSAAECAFVTGLTGLDHSKCOLYHSSCTSLTSGDGTGQCYKTACSYATGNTCANSVOG 1046

QY 280 TCATEQSRLR--AYLGLIGTAMT-----PNFVSNV----- 309
Db KCFDDATDCLRFANCASITGTLNTICVTYDPGCVANVNGTACQEKLATCAAYLTQNSC 1106

QY 310 -TSVALSCTCRGS-----GNLQECMELEGFFSHNPCLTEAIAA 347
Db STTAGTCAWSGSACLTVDVANVATECAVITG-----TGLTNAICA 1147

RESULT 10
T10053
laminin alpha 5 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10053
R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z16923
A;Accession: T10053
A;Status: preliminary; translated from GB/EMBL/DBEJ
A;Molecule type: mRNA
A;Residues: 1-3635 <MIN>
A;Cross-references: UNIPROT:Q61001; UNIPARC:UPI000004C5B8; EMBL:U37501; NID:g2599231; PIDN:
C;Genetics:
A;Gene: Lama5
C;Keywords: basement membrane; cell binding; extracellular matrix
F;1888-1939/Domain: laminin-type EGF-like homology <LEG>
F;1942-1970/Domain: EGF homology <EGF>

Query Match 5.3%; Score 116; DB 2; Length 3635;
Best Local Similarity 21.0%; Pred. No. 1.1;
Matches 87; Conservative 35; Mismatches 160; Indels 132; Gaps 21;

QY 7 RRLPPVVMILLLLP-PSPIPLAAGDPL-----PTESRLMNSCLQARRKQCDPTCSAAY 61
Db 1148 KPFPQPIILKDCQVLPPLPDLPLTQSBLSGAPPEGP-----QRPPTAVDPNAEPTL 1201

QY 62 HHLDSTSSISPLPS-----EPSVPADCL-----EAAQLRNSSL-----IG 100
Db 1202 LRHPGTVVFTTQVPTGLRYAFLLHGYQPVHPSPFVEVLINGRGIWQGHANASFCPHGVG 1261

QY 101 CMCHRRMKNQVACLDIYTVHRARSLGNYELDVSPYEDTVTSKPKMNL SKLN--MLKPD 158
Db 1262 C-----RTLVLG-----EGQTMLDVTDNELTIVTVRVEGRWLMDYVLIVPE 1303

QY 159 SDLCUKFAMLCVNLKCDRLRKA-----YGEACSPHCORHVCLRLQLLTFPEKAAP-- 210
Db 1304 DAYSSSYLQEEPLDKSYDFISHCATQGYHISPSSSSPFCRN--AATSLSLFYNNGALPCG 1361

QY 211 -HAQGLL-----LCPCA-----PNDR--GCGERRNTIAPNCA 240
Db 1362 CHEVGAVSPTCEPFGGQCPGRGHVIGRDCRCATGYWFPNCRPCDCCGARLDELGTGQCI 1421

QY 241 LPP--VAPNCLRLRLCFSDPLCRSRLVDFQTHCHPMILG-----TC 281
Db 1422 CPRTVPDPCLVCQPSFG-----CHP--LVGCECNCSPGVQELTDPDTC 1465

QY 282 ATE--QSRCLRAYLGLIGTAMTPNFVNNTSVLSCTCRGSGNLOECMELEG 333
Db 1466 DMDSGQCRPNVAGRCDDTCAPGYGYPS---CRPCDCEAGTMAWVCDPLTG 1516

RESULT 11
A46019
notch-1 protein - mouse
N;Alternate names: notch protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gri
Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
A;Reference number: A46019; MUID:93194170; PMID:849489
A;Accession: A46019
A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2531
A;Cross-references: UNIPROT:Q01705; UNIPARC:UPI00002922B; GB:S47228; NID:g2.
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
submitted to the EMBL Data Library, April 1992
A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, sugges
A;Reference number: S25144
A;Accession: S25144
A;Molecule type: mRNA
A;Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <PRA>
A;Cross-references: UNIPARC:UPI0000177461; EMBL:Z11886
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety
A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: C49175
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1161-1547 <LAR>
A;Cross-references: UNIPARC:UPI0000177462; EMBL:X68278; NID:g287987; PIDN:CAA48339.1; P
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126159)
R;Kopan, R.; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinat
A;Reference number: A46438; MUID:93252998; PMID:8486742

A/Accession: B46438
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054
A/Cross-references: UNIPARC:UPI0000177463
A/Experimental source: embryo
A/Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIPI:131247)
C/Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.
C/Comment: This protein is one of the neurogenic proteins controlling the decision between
C/Genetics:
A/Gene: notch-1
A/Map position: 2
A/Note: proximal region of chromosome 2
C/Superfamily: notch protein; ankyrin repeat homology; EGF homology
F/106-138/Domain: EGF homology <EGF1>
F/144-175/Domain: EGF homology <EGF1>
F/222-254/Domain: EGF homology <EGF2>
F/261-292/Domain: EGF homology <EGF2>
F/339-370/Domain: EGF homology <EGF3>
F/416-449/Domain: EGF homology <EGF3>
F/456-487/Domain: EGF homology <EGF3>
F/494-525/Domain: EGF homology <EGF4>
F/532-563/Domain: EGF homology <EGF4>
F/607-638/Domain: EGF homology <EGF4>
F/682-713/Domain: EGF homology <EGF4>
F/757-788/Domain: EGF homology <EGF4>
F/795-826/Domain: EGF homology <EGF4>
F/873-904/Domain: EGF homology <EGF4>
F/911-942/Domain: EGF homology <EGF4>
F/949-980/Domain: EGF homology <EGF4>
F/987-1018/Domain: EGF homology <EGF4>
F/1025-1056/Domain: EGF homology <EGF4>
F/1063-1094/Domain: EGF homology <EGF4>
F/1149-1180/Domain: EGF homology <EGF4>
F/1187-1218/Domain: EGF homology <EGF4>
F/1233-1264/Domain: EGF homology <EGF4>
F/1352-1383/Domain: EGF homology <EGF4>
F/1391-1425/Domain: EGF homology <EGF4>
F/1917-1948/Domain: ankyrin repeat homology <AN1>
F/1949-1981/Domain: ankyrin repeat homology <AN2>
F/1983-2015/Domain: ankyrin repeat homology <AN3>
F/2016-2048/Domain: ankyrin repeat homology <AN4>
F/2049-2081/Domain: ankyrin repeat homology <AN5>

RESULT 12
T42215
zonadhesin - mouse
N/Alternate names: sperm-specific membrane protein
C/Species: Mus musculus (house mouse)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42215
R/Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A/Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
A/Reference number: Z22080; MUID:98123114; PMID:9452463
A/Accession: T42215
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-5376 <GAO>
A/Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15B; EMBL:U97068; NID:G3327420; P
C/Genetics:
A/Gene: Zan
A/Map position: 5
C/Function:
A/Description: functions in multiple cell adhesion processes
A/Note: found exclusively on the apical region of the sperm head
C/Keywords: cell adhesion

Query Match 5.3%; Score 115; DB 2; Length 5376;
Best Local Similarity 21.1%; Pred. No. 2;
Matches 80; Conservative 30; Mismatches 132; Indels 138; Gaps 19;

QY 42 NSCLQARRKQADPTCSAAYHLLDCTSSISTPLPSEEPSVPADCLEAAQQLNSSLIGC 101
Db 3291 SNCTEITLQC---PTNSQFTDCLPSCVPCSNRCRVTSPSPSSCRE-----GC 3336
QY 102 MCHRRM-----KNQVACLDIYVTVHRRASLGNLYELDVSPYEDVTVTSKPKWM----- 147
Db 3337 LCNHGFVSEDKCVPTQCGKD-----ARGA-----IIPAGTWTISKGCTQSCACV 3383
QY 148 --NLSKLNMLKP-----DSDLCLKPFAMLTINDK-----PNCALPPVAPNCLERRLC- 255
Db 3384 EGNIOCNFQCPPEYCKDNSEGSTCTKITLQCPAHTQVTSCLPCLSPCLDPEGLCKD 3443
QY 178 LRKAYGEAC-SGPHQQRHVCLRQLLTFFFEKAAE-PHAQGLL----- 217
Db 3444 ISKVPSTCKEGCVCQSGVYLSNDSKCVLRAEDCKDAQAGALIPAGKTWTSPGCTQSCACM 3503
QY 218 -----CP-----CAPNDRGCGERRNTIA-----PNCALPPVAPNCLERRLC- 255
Db 3504 GGAVQCQSQCPPEYCKDNSEGSTCTKITLQCPAHTQVTSCLPCLSPCLDPEGLCKD 3562
QY 256 FSDP-----LCRSRLVDFQTHCHPMDILGTQCATQSQRCRLRAYLGLIGTAMTPNFV 305
Db 3563 GASPKVPSTCKEGCVCQSGVYLSNDSKCVLRAEDCKDAQAGALIPAGKTWTSPGCTQSCACM 3609
QY 306 SNVNTSVALSCYCRSGNLIQ 325
Db 3610 TWSRGCTQSCVCTG-GSIQ 3628

RESULT 13
T44598
hypothetical protein [imported] - fruit fly (Drosophila melanogaster)
N/Alternate names: BcDNA.LD22726
C/Species: Drosophila melanogaster
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Nov-2000
C/Accession: T44598
R/Rubin, G.M.; Wan, K.H.; Harvey, D.; Lewis, S.E.; Brokstein, P.; Tsang, G.; Agbayani, M.;
n, D.E.; Frise, E.; Galle, R.; George, R.A.; Harris, N.L.; Hoskins, R.A.; Evans-Holm, M.;
Snit, E.; Svirskas, R.R.; Weinburg, T.; Celnikier, S.E.
submitted to the EMBL Data Library, April 1999
A/Reference number: Z22805
A/Accession: T44598
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1106 <RUB>

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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:00:03 ; Search time 154.078 Seconds
(without alignments)
1831.616 Million cell updates/sec

Title: US-10-668-936-21

Perfect score: 2190

Sequence: 1 MVRPLNRPPLPPVLMLLL.....PWVPSLFSCTPLILLLSLW 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2190	100.0	400	1	GFR33 HUMAN
2	1646.5	75.2	397	1	GFR33 MOUSE
3	1642.5	75.0	397	2	G6AXR3 RAT
4	1628	74.3	385	2	Q9R2D0 MOUSE
5	1051	48.0	222	2	Q9QZG2 RAT
6	568	25.9	465	1	GFR33 CHICK
7	545.5	24.9	463	2	Q920Y3 MOUSE
8	545.5	24.9	464	2	Q5E9X0 BOVIN
9	544.5	24.9	463	1	GFR33 MOUSE
10	542.5	24.8	444	2	Q792X9 RAT
11	542.5	24.8	464	2	Q35977 RAT
12	540.5	24.7	460	2	Q5REZ9 PONPY
13	540.5	24.7	464	1	G6GTR9 HUMAN
14	540.5	24.7	464	2	Q5RAD6 PONPY
15	540.5	24.7	464	2	Q5RAD6 PONPY
16	536.5	24.5	469	1	GFR33 CHICK
17	530.5	24.2	464	2	Q5R9T3 PONPY
18	529.5	24.2	431	2	Q4RG88 TETNG
19	522.5	23.9	472	2	Q98TT9 BRARE
20	516	23.6	465	1	GFR33 HUMAN
21	514.5	23.5	463	2	Q35252 MOUSE
22	513	23.4	468	1	GFR33 MOUSE
23	513	23.4	468	2	Q35246 MOUSE
24	512.5	23.4	463	2	Q35748 RAT
25	511	23.3	468	1	GFR33 RAT
26	504	23.0	481	2	Q98TT8 BRARE
27	497.5	22.7	431	1	GFR33 CHICK
28	496	22.6	333	2	Q4RTG0 TETNG
29	482.5	22.0	495	2	Q6TSC3 BRARE
30	474.5	21.7	342	2	Q4SDM1 TETNG
31	454.5	20.8	484	2	Q4S1R4 TETNG

32	418.5	19.1	358	2	Q922A3 MOUSE	Q922A3 mus musculus
33	412.5	18.8	359	2	Q58J92 HUMAN	Q58J92 homo sapien
34	408	18.6	330	2	Q922A2 MOUSE	Q922A2 mus musculus
35	406	18.5	203	2	Q4SEK7 TETNG	Q4SEK7 tetraodon n
36	361.5	16.5	260	1	GFR33 MOUSE	Q9JIT2 mus musculus
37	361	16.5	273	1	GFR33 RAT	Q9SEI2 rattus norv
38	296.5	13.5	299	1	GFR33 HUMAN	Q9GZ27 homo sapien
39	296.5	13.5	299	2	Q5JT74 HUMAN	Q5JT74 homo sapien
40	275.5	12.6	247	2	Q4SG83 TETNG	Q4SG83 tetraodon n
41	257.5	11.8	182	2	Q5JT77 HUMAN	Q5JT77 homo sapien
42	220	10.0	394	2	Q6UXV0 HUMAN	Q6UXV0 homo sapien
43	219	10.0	393	2	Q6SJE0 MOUSE	Q6SJE0 mus musculus
44	210	9.6	225	2	Q9QWK2 MOUSE	Q9QWK2 mus musculus
45	184.5	8.4	109	2	Q8JG58 AMBME	Q8JG58 ambystoma m

ALIGNMENTS

RESULT 1

GFR33 HUMAN

ID GFR33 HUMAN STANDARD; PRT; 400 AA.

AC O60603; O6UM20; Q8IUZ2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).

OS Name=GFR33; ORFName=UNQ339/PRO538/PRO3664;

GN Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND TISSUE SPECIFICITY.

RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Baloh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,

RA Popescu N.C., Johnson E.M. Jr., Milbrandt J.;

RA "GFRalpha3 is an orphan member of the GDNF/neurturin/persephin

RT receptor family."

RL Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806 (1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).

RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Kimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri R.L., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

RA Yaneura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RA "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RL bioinformatics assessment."

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RA TISSUE=Pancreas;

RA MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RN PROTEIN SEQUENCE OF 32-46.
RP PubMed=15340161; DOI=10.11110/ps.04682504;
RX Zhang Z., Henzel W.J.;
RA "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [5]
RN FUNCTION.
RX MEDLINE=99098192; PubMed=9883723; DOI=10.1016/S0896-6273(00)80649-2;
RA Baloh R.H., Tansey M.G., Lampe P.A., Fahrner T.J., Enomoto H.,
RA Simburger K.S., Leitner M.L., Araki T., Johnson E.M. Jr.,
RA Milbrandt J.;
RT "Artemin, a novel member of the GDNF ligand family, supports
RT peripheral and central neurons and signals through the GFRalpha3-RET
RT receptor complex.";
RL Neuron 21:1291-1302(1998).
CC -I- FUNCTION: Receptor for the glial cell line-derived neurotrophic
CC factor, artemin. Mediates the artemin-induced autophosphorylation
CC and activation of the RET receptor tyrosine kinase.
CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -I- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O60609-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O60609-2; Sequence=VSP_010942;
CC -I- TISSUE SPECIFICITY: Widely expressed in adult and fetus which
CC exhibit a similar pattern. Essentially not expressed in the
CC central nervous system, but highly expressed in several sensory
CC and sympathetic ganglia of the peripheral nervous system. Moderate
CC expression in many nonneuronal tissues, particularly those of the
CC digestive and urogenital systems, but high expression in stomach
CC and appendix. Several types of glandular tissues show low
CC expression. Very low or no expression detected in the
CC hematopoietic system.
CC -I- SIMILARITY: Belongs to the GDNFR family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF051767; AAC24355.1; -; mRNA.
CC EMBL; AV358997; AAQ89356.1; -; mRNA.
CC EMBL; AV359037; AAQ89396.1; -; mRNA.
CC EMBL; BC037951; AAH37951.1; -; mRNA.
CC Ensemble; ENSG00000146013; Homo sapiens.
CC HGNC; HGNC:4245; GFR3.
CC MIM; 605710; -.
CC GO; GO:0019898; TAS.
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007422; P:peripheral nervous system development; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC GO; GO:0003438; GDNF receptor.
CC InterPro; IPR003505; GDNF_receptor3.
CC PANTHER; PTHR10269; GDNF_Receptor; 1.
CC Pfam; PF02351; GDNF; 1.
CC PRINTS; PR01319; GDNFRALPHA3.
CC PRINTS; PR01316; GDNFRECEPTOR.
CC Alternative splicing; Direct protein sequencing; Glycoprotein;
KW GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
FT SIGNAL 1 31
FT CHAIN 32 374 GDNF family receptor alpha 3.

FT PROPEP 375 400 Removed in mature form (Potential).
FT LIPID 374 374 GPI-anchor amidated asparagine
FT CARBOHYD 95 95 (Potential).
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 309 309 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 127 157 Missing (in isoform 2).
FT CONFLICT 108 108 /FTId=VSP_010942.
FT SEQUENCE 400 AA; 44511 MW; B0BC252FE1F072C7 CRC64;
SQ
Query Match 100.0%; Score 2190; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.9e-168;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVRPLNRPPLPPVLMMLLLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
DB 1 MVRPLNRPPLPPVLMMLLLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
QY 61 YHLLDSCTSSISTPLPSPSEPSVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120
DB 61 YHLLDSCTSSISTPLPSPSEPSVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120
QY 121 HRASISGNLYELDVSPYEDVTVTSKPMKNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRK 180
DB 121 HRASISGNLYELDVSPYEDVTVTSKPMKNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRK 180
QY 181 AYGEACSGPHCQRHVCLRLQLLTFFEKAAEPHAQGLLLCPCAPNDRCGRRRTIAPNCA 240
DB 181 AYGEACSGPHCQRHVCLRLQLLTFFEKAAEPHAQGLLLCPCAPNDRCGRRRTIAPNCA 240
QY 241 LPPVAPNCLRLRRLCFSDPLCRSLRVDFTCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
DB 241 LPPVAPNCLRLRRLCFSDPLCRSLRVDFTCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRGSLNQECEMLEGFFSHNPLCTEATIAAKRHFHSQSFQDW 360
DB 301 TPNFVSNVNTSVALSCTCRGSLNQECEMLEGFFSHNPLCTEATIAAKRHFHSQSFQDW 360
QY 361 PHTFAVMAHQENPAVRPQWPVPSLFTPLILLLSLW 400
DB 361 PHTFAVMAHQENPAVRPQWPVPSLFTPLILLLSLW 400
RESULT 2
GFR3_MOUSE
ID GFR3_MOUSE STANDARD; PRT; 397 AA.
AC O35118; O35325; O55243; Q6NZC2; Q8C8L9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).
GN Names=Gfra3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Heart;
RX MEDLINE=98205811; PubMed=9535755; DOI=10.1006/bbrc.1998.8361;
RA Nomoto S., Ito S., Yang L.-X., Kiuchi K.;
RT "Molecular cloning and expression analysis of GFR alpha-3, a novel
RL cDNA related to GDNFR alpha and NTRN-alpha".
RL Biochem. Biophys. Res. Commun. 244:849-853(1998).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=98420233; PubMed=9749804;
RA Widenfalk J., Tomac A., Lindqvist E., Hoffer B., Olson L.;
RT "GFRalpha-3, a protein related to GFRalpha-1, is expressed in
RT developing peripheral neurons and ensheathing cells".
RL Eur. J. Neurosci. 10:1508-1517(1998).


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QY 189 PHCQRHVLCRLQLTFPEKAAEPHAQGLLCPAPNDRGCGERRNTIAPNCALPPVAPNC 248
DB 186 IRCQRLCLQAQLRSFPEKAAESHAQGLLCPAPNDRGCGERRNTIAPSCALPSVTPNC 245
QY 249 LEIIRLRCFSDPLCRSLRVDFOTHCHPMDILGTCAEQSLRAYLGLIGTAMTPNVSNU 308
DB 246 LDLRSFCRADPLCRSLRMDFOTHCHPMDILGTCAEQSLRAYLGLIGTAMTPNFIKV 305
QY 309 NTSVALSCTCRSGNLQCECEMLEGFFSHNPCLTEIAAAMRPHSOLFQDMPHPTFAVM 368
DB 306 NITVALSCTCRSGNLQCECEQLERSFSQNPCLVEIAAAMRPHRQLFSQDWDADSTFSVV 365
QY 369 AHQONENPAVRPQWVPSLFTPLILLISLW 400
DB 366 QQQNSNPALRLOPLRPILSFSILPLILLQTLW 397

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RESULT 3
Q6AXR3 RAT PRELIMINARY; PRT; 397 AA.
AC Q6AXR3;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Glial cell line derived neurotrophic factor family receptor alpha
DE 3.
GN Names=Gfra3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079378; AAH79378.1; -, mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 397 AA; 44053 MW; E11D2E7B9CB46AF8 CRC64;

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Query Match 75.08; Score 1642.5; DB 2; Length 397;

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Best Local Similarity 77.2%; Pred. No. 9e-124;
Matches 305; Conservative 30; Mismatches 57; Indels 3; Gaps 1;

QY 6 NRPPLPPVVLMLLLPLPSPLPLAAGDPLPTSRMLNMSCLOARRKCOADPTCSAAHYHLD 65
DB 6 SPRPPLVILLVLSL--WLPGLTGNLSPTENRLVNSCTQARKKCEANPACKAAAYQHLD 62
QY 66 STTSISITPLSEEPSVPADCLAAQAQLRNSSLIGCMCHRRMKNQVACLDIYTVVHRAS 125
DB 63 SCTPSLSSPLPSGESATSAAACLEAAQAQLRNSSLIDCRHRRMKHQTCLDIIYTVVHVS 122
QY 126 LGNYELDVSPYEDTIVTSKPKWKNLKLKMLKPDSDCLKFAMLCITLNDKCDRLRKAYGEA 185
DB 123 LGDYELDVSPYEDTIVTSKPKWKNLKLKMLKPDSDCLKFAMLCITLNDKCDRLRKAYGEA 182
QY 186 CSGPHCQRHVLCRLQLTFPEKAAEPHAQGLLCPAPNDRGCGERRNTIAPNCALPPVA 245
DB 183 CSGIRQCRLCLQAQLRSFPEKAAESHAQGLLCPAPNDRGCGERRNTIAPSCALPSVA 242
QY 246 PNCLELRRLCFSDPLCRSLRVDFOTHCHPMDILGTCAEQSLRAYLGLIGTAMTPNFV 305
DB 243 PNCLELRSLFCRADPLCRSLRMDFOTHCHPMDILGTCAEQSLRAYLGLIGTAMTPNFI 302
QY 306 SNVNTSVALSCTCRSGNLQCECEMLEGFFSHNPCLTEIAAAMRPHSOLFQDMPHPTTF 365
DB 303 SKVNTVALGCTCRSGNLQCECEQLERSFSQNPCLVEIAAAMRPHRQLFSQDWDADSTF 362
QY 366 AVMAHQENENPAVRPQWVPSLFTPLILLISLW 400
DB 363 SVMQQNSNPALRLOPLRPILSFSILPLILLQTLW 397

RESULT 4
Q9R2D0 MOUSE PRELIMINARY; PRT; 385 AA.
AC Q9R2D0;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DE TGF-beta-related neurotrophic receptor-3 precursor.
GN Names=Gfra3; Synonyms=Trnr-3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Swiss-Webster /NIH; TISSUE=Embryo;
RA Zhong J., Annies M., Tolle A., Heumann R.;
RT "Molecular cloning of a new member of Trnr family.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15110; CAAY5384.1; -, mRNA.
DR MGI; MGI:1201403; Gfra3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IMP.
DR GO; GO:0007422; P:peripheral nervous system development; IMP.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003505; GDNF_receptorA3.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01319; GDNFRALPHA3.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor; Signal.
FT SIGNAL 1 15 Potential.
SQ SEQUENCE 385 AA; 42997 MW; 91A7F3P9FF30ED14 CRC64;

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Query Match 74.3%; Score 1628; DB 2; Length 385;
 Best Local Similarity 77.9%; Pred. No. 1.3e-122;
 Matches 300; Conservative 29; Mismatches 56; Indels 0; Gaps 0;


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FT CONFLICT 462 462 Q -> L (in Ref. 3).
SQ SEQUENCE 464 AA; 51559 MW; 8BC604D9530FF21F CRC64;

Query Match 24.7%; Score 540.5; DB 1; Length 464;
Best Local Similarity 36.5%; Pred. No. 5.2e-35;
Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

QY 44 CLOARRKCOADPTCSAAVHHLDSCS--SISPLSEEPSVPADCLEAAQQLRNSSLIGC 101
DB 40 CVRANELCAAESNCSSRYRTLQCLAGDRDNTMLANKE-----COAALEVLQESPLYDC 93

QY 102 MCHRRMKNOVACLDIYWTVHRARSIGNYELDVSPYEDVTTSKPKWKNLSKL----- 152
DB 94 RCKRGKKELQCLQIYWSIHGLGTEGEFFYASPYE--PVTSR-----LSDIFRLASIFSG 147

QY 153 -----NMLKPDSDLCIKFAMLCITLNDKDLRKAYGEACS-----GPHQORHVCLRLQTLTF 203
DB 148 TGADFPVSAKSNHCLDAAKACNLNDNCKLRSSYSICNREISPTERCNRRKCHKALRQF 207

QY 204 FEKAAPHAQGLLCPAPNDRGCGERRRNTIAPNCAL--PPVAPNCLRLRLCFDPLCR 262
DB 208 FDRVPSEYTYRMLFCSC--ODQACAEERRQTILPSCSYEDKEKPNCLDLRGVCRTHLCL 265

QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALS--CTC 318
DB 266 SRLADPHANCRAASYQTVTSCPADNYQACLGSGAGMIGFDMTNYVDSSPTGIIVSPWCSC 325

QY 319 RSGNLOQECMELEGFFSHNPLCTEIAIA 347
DB 326 RSGNMEECFKFLRDFTENPCLRNAIOA 354

RESULT 14
Q6GTR9 HUMAN PRELIMINARY; PRT; 464 AA.
AC Q6GTR9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE GDNF family receptor alpha 2, preproprotein.
GN Name=GFPRA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Caesavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
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RA Director MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041688; AAH41688.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 464 AA; 51543 MW; 8BC61529530FF21F CRC64;

Query Match 24.7%; Score 540.5; DB 2; Length 464;
Best Local Similarity 36.5%; Pred. No. 5.2e-35;
Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

QY 44 CLOARRKCOADPTCSAAVHHLDSCS--SISPLSEEPSVPADCLEAAQQLRNSSLIGC 101
DB 40 CVRANELCAAESNCSSRYRTLQCLAGDRDNTMLANKE-----COAALEVLQESPLYDC 93

QY 102 MCHRRMKNOVACLDIYWTVHRARSIGNYELDVSPYEDVTTSKPKWKNLSKL----- 152
DB 94 RCKRGKKELQCLQIYWSIHGLGTEGEFFYASPYE--PVTSR-----LSDIFRLASIFSG 147

QY 153 -----NMLKPDSDLCIKFAMLCITLNDKDLRKAYGEACS-----GPHQORHVCLRLQTLTF 203
DB 148 TGADFPVSAKSNHCLDAAKACNLNDNCKLRSSYSICNREISPTERCNRRKCHKALRQF 207

QY 204 FEKAAPHAQGLLCPAPNDRGCGERRRNTIAPNCAL--PPVAPNCLRLRLCFDPLCR 262
DB 208 FDRVPSEYTYRMLFCSC--ODQACAEERRQTILPSCSYEDKEKPNCLDLRGVCRTHLCL 265

QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALS--CTC 318
DB 266 SRLADPHANCRAASYQTVTSCPADNYQACLGSGAGMIGFDMTNYVDSSPTGIIVSPWCSC 325

QY 319 RSGNLOQECMELEGFFSHNPLCTEIAIA 347
DB 326 RSGNMEECFKFLRDFTENPCLRNAIOA 354

RESULT 15
QSRAD6 PONPY PRELIMINARY; PRT; 464 AA.
AC QSRAD6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp459C0228.
GN Name=DKFZp459C0228;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RA Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR859081; CAH91274.1; -, mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51560 MW; 46441C50299CCCPA CRC64;

Query Match 24.7%; Score 540.5; DB 2; Length 464;
Best Local Similarity 36.5%; Pred. No. 5.2e-35;
Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

QY 44 CLOARRKCOADPTCSAAVHHLDSCS--SISPLSEEPSVPADCLEAAQQLRNSSLIGC 101
DB 40 CVRANELCAAESNCSSRYRTLQCLAGDRDNTMLANKE-----COAALEVLQESPLYDC 93
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:12:04 ; Search time 19.5734 Seconds
(without alignments)
959.442 Million cell updates/sec

Title: US-10-668-936-21
Perfect score: 2190
Sequence: 1 MVRPLNRPPLPPVVLMLLL.....PWVPSLFSCTPLILLISLW 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
8: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
10: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1646.5	75.2	397	11	US-11-253-151-33
2	542.5	24.8	444	11	US-11-253-151-34
3	540.5	24.7	464	9	US-10-745-586-112
4	511	23.3	468	11	US-11-253-151-35
5	497.5	22.7	431	11	US-11-253-151-32
6	361	16.5	258	11	US-11-253-151-9
7	361	16.5	273	11	US-11-253-151-8
8	132	6.0	580	11	US-11-183-136-8
9	129	5.9	1057	11	US-11-149-003-6
10	129	5.9	1251	11	US-11-149-003-16
11	129	5.9	1342	11	US-11-149-003-24
12	129	5.9	1512	11	US-11-149-003-10
13	129	5.9	1570	11	US-11-149-003-12
14	129	5.9	1628	11	US-11-149-003-2
15	123.5	5.6	2871	9	US-11-169-041-131
16	123.5	5.6	3002	9	US-10-821-234-916
17	123	5.6	999	11	US-11-113-424-36
18	123	5.5	1170	11	US-11-114-962-5
19	119.5	5.5	997	11	US-11-113-424-37
20	117.5	5.4	508	9	US-10-915-160-2
21	116	5.3	3635	11	US-11-019-711-47

22	115	5.3	451	9	US-10-915-160-6	Sequence 6, Appli
23	114.5	5.2	470	9	US-10-915-160-4	Sequence 4, Appli
24	114	5.2	1433	11	US-11-114-962-1	Sequence 1, Appli
25	113.5	5.2	1192	11	US-11-149-003-18	Sequence 18, Appl
26	113.5	5.2	1207	11	US-11-149-003-20	Sequence 20, Appl
27	113.5	5.2	1477	11	US-11-149-003-8	Sequence 8, Appli
28	113.5	5.2	1535	11	US-11-149-003-14	Sequence 14, Appl
29	113.5	5.2	1566	9	US-10-453-372-1190	Sequence 1190, Ap
30	113.5	5.2	1593	11	US-11-149-003-4	Sequence 4, Appli
31	113.5	5.2	2026	8	US-10-505-928-831	Sequence 831, App
32	112.5	5.1	2556	11	US-11-050-346-67	Sequence 67, Appl
33	112	5.1	997	11	US-11-080-991-50	Sequence 50, Appl
34	111.5	5.1	434	11	US-11-241-956-5	Sequence 5, Appli
35	111.5	5.1	1609	11	US-11-072-175-185	Sequence 185, App
36	111	5.1	2440	9	US-10-766-317-10	Sequence 10, Appl
37	110	5.0	4544	9	US-10-501-035-214	Sequence 214, App
38	110	5.0	4544	11	US-11-076-427A-32	Sequence 32, Appl
39	109	5.0	580	11	US-11-183-136-6	Sequence 6, Appli
40	109	5.0	580	11	US-11-046-653-2	Sequence 2, Appli
41	109	5.0	2471	11	US-11-050-346-68	Sequence 68, Appl
42	108.5	5.0	1544	9	US-10-453-372-1186	Sequence 1186, Ap
43	108.5	5.0	1565	9	US-10-453-372-1180	Sequence 1180, Ap
44	108.5	5.0	2053	9	US-10-453-372-1174	Sequence 1174, Ap
45	108.5	5.0	2143	9	US-10-453-372-1188	Sequence 1188, Ap

ALIGNMENTS

RESULT 1

US-11-253-151-33
; Sequence 33, Application US/11253151
; Publication No. US20060069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; PRIOR FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 33
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-253-151-33

Query Match	75.2%	Score 1646.5	DB 11	Length 397
Best Local Similarity	77.8%	Pred. No. 2.1e-142		
Matches 305	Conservative 30	Mismatches 56	Indels 1	Gaps 1
QY	9	PLPPVVLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAAVHLLDSC	68	
Db	7	PRPP-LMLILLVLSLWPLGNSLATENRFVNSTQARKKCEANPACKAAVOHLSCT	65	
QY	69	SSISTPLPSEEPSVADCLAAQOLRNSSLIIGCMCHRMKNQVACLDIYVTVHARSLSGN	128	
Db	66	SSLSRPLPLESAMSDCLAEAEQLNSSLIDCRCHRMKHQATCLDIYVTVHPARSLGD	125	
QY	129	YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDICLKPFAMLCITLNDKCDRLRKAYGEACSG	188	
Db	126	YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDICLKPFAMLCITLNDKCDRLRKAYGEACSG	185	
QY	189	PHCORHVLQRLTLTFEKAEPHAQGLLCPCAPNDRGCGGERRRNTIAPNCALPPVPAPNC	248	
Db	186	IRCQRHLCAQURSKFFFEKAESHAQGLLCPCAPNDRGCGGERRRNTIAPSCALPSPVTPNC	245	

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QY 249 LELRLCFSDPLCRSLVDFOQHCHPMDILGTCATEQSCRLAYLGLIGTAMTNPFSNV 308
DB 246 LDRSFCRADPLCRSLMDFOQHCHPMDILGTCATEQSCRLAYLGLIGTAMTNPFSKV 305
QY 309 NTSVALSCTCRSGNLQECMELEGFSFNPCLTETAAAKMRFHSLQFSQDWPHTFFAM 368
DB 306 NTVVALSCTCRSGNLQECMELEGFSFNPCLTETAAAKMRFHSLQFSQDWDSTFSV 365
QY 369 AHQNPENAVRQPPWPSLSCSLPLILLSLW 400
DB 366 QQQNSNPALRQPLRPLILSILPLILLQTLW 397

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RESULT 2

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US-11-253-151-34
; Sequence 34, Application US/11253151
; Publication No. US20060069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 34
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-253-151-34

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Query Match 24.8%; Score 542.5; DB 11; Length 444;
Best Local Similarity 37.4%; Pred. No. 1.2e-41;
Matches 123; Conservative 42; Mismatches 125; Indels 39; Gaps 10;

QY 44 CLOARRKCOADPTCSAAVHHLDSCTS--SISTPLPSEEPSVPADCLEAAQQLRNSSLIGC 101
DB 40 CVRANELCAAESCSRYRTLQCLAGDRDNTMLANKE-----COAALEVLQESPLYDC 93
QY 102 MCHRRMKNQVACLDIYTWTHRRARSLGNYELDVSPYEDTVTSPKWNLSKLNML----- 155
DB 94 RCKRGMKKELQCLQIYWSIHGLTEGEEFYEAAPYE-PVTSR-----LSDIFRLASIFSG 147
QY 156 -----KPSDILCLKFMCLTNDKCDRLRKAYGEACS-----GPHCQHVCLRLQLTF 203
DB 148 TGTDPVAVSTKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRRKCHKALROF 207
QY 204 FEKAEPHAQGLLLCPAPNDRCGERRRNTIAPNCAL-PPVAPNCLLELRLLCFSDPLCR 262
DB 208 FDRVPSEYTYRMLFCSG--QDQACABRRRQTLPLSCSYEDKEKPNCLDLRGVCRTHLCL 265
QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTNPFSNVNNTSVALS--CTC 318
DB 266 SRLADFHANCRAASYRTITSCPADNYOACLGSYAGMIGFDMTPNYVDSPNPTGIIVVSPWCNC 325
QY 319 RGSNGNLQECMELEGFPFSHPNCLTEAIAA 347
DB 326 RGSNGNMEECCKFLRDFTENPCLRNAIQA 354

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RESULT 4

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US-11-253-151-35
; Sequence 35, Application US/11253151
; Publication No. US20060069242A1
; GENERAL INFORMATION:
; APPLICANT: MASURE, STEFAN L.J.
; APPLICANT: CIK, MIROSLAV
; APPLICANT: HOEFNAGEL, EVERT W.
; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 35
; LENGTH: 468
; TYPE: PRT

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RESULT 3

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US-10-745-586-112
; Sequence 112, Application US/10745586
; Publication No. US20060063227A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.

```



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; TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: JAB-1512
; CURRENT APPLICATION NUMBER: US/11/253,151
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/04918
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 9915200.1
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-253-151-8

Query Match      16.5%; Score 361; DB 11; Length 273;
Best Local Similarity 34.3%; Pred. No. 2.5e-25;
Matches 87; Conservative 25; Mismatches 102; Indels 40; Gaps 8;

QY 145 WKNLKSLNMLKPSDLDLCKFAMLTLDKCDRLRKAYGEACG-----PHCQHVCL 197
Db 20 WSLGQCGSASSTEGNRCVVEAAEACTADQCQQLRSEYVAQCLGRAGWPGSCVRSRCR 79
QY 198 ROLLTFEKAAPHAQGLLLCPCAPNDRCGGERRRNTIAPNCAL--PPVA-PNCLELRRL 254
Db 80 RALRRFFARGPPALTHALLFCGC--EGPACAEERRQTAPACAFSGPQLAPPSCCLKPLDR 137
QY 255 CFSDDLRSRLVDQTHCHPMILGT---CATEQS-RLRAYLGLIGTAMTNPVSNVT 310
Db 138 CERSRRCPRLFAFQASCAPAP--GSRDCCPEGGPRCLRAYAGLVGTVTNYLDNWSA 195
QY 311 SVALSCTCRSGNLOCEMBLGGFFSHNPCLTEAIAAKMRFHSQLFSDQWPHPTFAVMAH 370
Db 196 RVAPWCGCEASGNRRECEAFKLTFRNCLDGA-----QAF 233
QY 371 QNENPAVRPQWVP 384
Db 234 DSSQPSVLQDQWNP 247

RESULT 8
US-11-183-136-8
; Sequence 8, Application US/11183136
; Publication No. US20060019896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Dean
; APPLICANT: Park, Kye Won
; TITLE OF INVENTION: NETRIN-RELATED COMPOSITIONS AND USES
; FILE REFERENCE: UUTH-P01-011
; CURRENT APPLICATION NUMBER: US/11/183,136
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: US 60/587,796
; PRIOR FILING DATE: 2004-07-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Mouse
US-11-183-136-8

Query Match      6.0%; Score 132; DB 11; Length 580;
Best Local Similarity 22.5%; Pred. No. 0.00047;
Matches 104; Conservative 40; Mismatches 194; Indels 124; Gaps 23;

QY 20 LLPSPPLPLAAGDPLPTESRLMNSCLQARKKCOADPTCSAAYHLD-----S 66
Db 97 LQAQAPFNVTLTVPGLKAFELVFVSL---RFSAPPTSVALLKSDHGRSWVPLGFSSS 153
QY 67 CTSSIS-TPLPSEPSVP---ADCLEAAQ-----QLRNSSLIGC 101
Db 154 CTLDYGLPAPADGPGSGFEALCFPAPQAPDGGGLLAFVSQDGGSPQGLDLNDSVP--- 210
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QY 102 MCHRRMKNQVACLIDYWTVHRRSLGNVELDVSFYEDVTTSKPMKMLSKLMLKPSDLD 161
Db 211 -----LQDWVTATDIRIVLTRPATQGD-----TRDGGVTVPFYSATLEQV--GGRCK 256
QY 162 CLKFAMLTLDK-----CDRLRKAYGEACGPHQQRHVCLRQLLTFPEKAAEPHAQGLLL 217
Db 257 CNGHASRCLLDTHGHLVCDCHQGTGEPDCS--RCKPFVCDRP---WQRATGQEAHACLA 310
QY 218 CPCAPNDRGC-----GERRNTIAPNCALPPVAPNCPNLELRRLCFSDP-----L 260
Db 311 CSCNGHARRCTCFNMELYRLSGRRSGVCLNCRHNTAGRHCHYCREGFFYRDPGRVLSDRRA 370
QY 261 CRSRLVDQTHCHPMILGT--TC--ATEQSRCLRAYLGLIGTAMTNPVSN-----VNT 310
Db 371 CRA-----CDCHPVGAAGKTCNQTGQCPKDGVTGLTCNRCAPGFGQFSRSPVAPCVKT 424
QY 311 SVALSCTCRSGNLOECEE-----MLGGFFSHNPCLTEAIAAKMRFHSQLFSDQ 358
Db 425 PVP-GPTESSPVPEQDCESHCRPARGSYRISLKKFCKRDYAVQVAVGARGEARG----- 478
QY 359 DWPHTTFVMA--HQNENPAVRPQP--WVPSL-FSCTLPLIL 395
Db 479 SWTRFPVAVLAVFRSGEERARRSSALWVPTLDAACGCPRL 520

RESULT 9
US-11-149-003-6
; Sequence 6, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding th
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-6

Query Match      5.9%; Score 129; DB 11; Length 1057;
Best Local Similarity 20.6%; Pred. No. 0.0018;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAYHLDSCSTSSISTP 74
Db 223 PDPREPCNLCTLGGFVTCTGRRPCBPBGCSHPLIPSGHCHCCPTCQGRYHGVTTASGETLP 282
QY 75 LPSEBSPVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLIDYWTVHRRSLGNLYBLDVS 134
Db 283 DPLDPTCSLCTCQEGSMRCQKKECAPALCPHSPGFCFP----VCHSCLSQGREHODGE 338
QY 135 FYEDVTTSKPM-KMNLKSLNMLKPSDLDLCKF---AMLCTL-----NDKCDRLR--KAYG 183
Db 339 EFEGPAGSCWCRCAQAGVS-----CVRLQCPPLPKLQVTERGSCPCRRCGLAHG 390
QY 184 E-----ACSGPHCQQRHVCLRQLLTTFFEKAAEPHAQGLLCP--CAPNDRGCG 228
Db 391 EEHPESGRVPPDPSACSSCVCHGVVTCARIQCISSCAQPR-QG-----PHDCCPQCSDC- 444
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QY 229 ERRNTIAPNCALPPVAPNCLLELRRLCFSDP-----LCRSLVDFQTHCHPMDIL-- 278
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
445 EHEGRKYEPGESFQFGADPC-----EVCICEPQEGPPSLRCHRRQCPSLVGCPPSOLLPP 500
QY 279 -----GTCATEQRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
501 GPOHCCPTCAEALNSCSE---GLLGSELAP-----PDCYTCQCQDLTWLCTHQACPE 550
QY 326 ECEMLEGFFSHNP-----CLTEATAAKMRHFSQLFSQDWPHTPTFAVMA----- 369
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
551 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACIACHTCHRG 602
QY 370 ----HONENPAVR--POPW--VPSLFSC 389
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
603 HVECHLEEQALSCPHGWAKVPOADSC 629

RESULT 10
US-11-149-003-16
; Sequence 16, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kielin-like Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1251
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-16

Query Match          5.9%; Score 129; DB 11; Length 1251;
Best Local Similarity 20.6%; Pred. No. 0.0022;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVYHLDSCSTSSISTP 74
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
417 PDPRECNLCCTCLGGFVTCGRPPCGSHPLIPSGHCCTCGCRYHGVTTASGETLP 476
QY 75 LPSEEPSVPADCLEAAQQLNSSLIGCMCHRRMKNQVACLDIYTVHRAARSLGNYELDVS 134
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
477 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGCFPCP-----VCHSCLSQGREHODGE 532
QY 135 PYEDTVTSKPW--KXNLSKLANMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
533 EFGPGAGSCWCRCQAGQVS-----CVRLQCPPLPKLVQTERGSCPCRCGCLAHG 584
QY 184 E-----ACSGPHCORHVCLRLQLLTFFKAAABPHAGLLCLCP--CAPNDRGCG 228
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
585 EEHPGSRWVPPDSACSSCVCHGVVTCARIQCISSCAQPR-QG-----PHDCCPQCSDC- 638
QY 229 ERRNTIAPNCALPPVAPNCLLELRRLCFSDP-----LCRSLVDFQTHCHPMDIL-- 278
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
639 EHEGRKYEPGESFQFGADPC-----EVCICEPQEGPPSLRCHRRQCPSLVGCPPSOLLPP 694
QY 279 -----GTCATEQRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
695 GPOHCCPTCAEALNSCSE---GLLGSELAP-----PDCYTCQCQDLTWLCTHQACPE 744
QY 326 ECEMLEGFFSHNP-----CLTEATAAKMRHFSQLFSQDWPHTPTFAVMA----- 369
```

```
Db 745 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACIACHTCHRG 796
QY 370 ----HONENPAVR--POPW--VPSLFSC 389
Db 797 HVECHLEEQALSCPHGWAKVPOADSC 823

RESULT 11
US-11-149-003-24
; Sequence 24, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kielin-like Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1342
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-24

Query Match          5.9%; Score 129; DB 11; Length 1342;
Best Local Similarity 20.6%; Pred. No. 0.0024;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVYHLDSCSTSSISTP 74
Db 508 PDPRECNLCCTCLGGFVTCGRPPCGSHPLIPSGHCCTCGCRYHGVTTASGETLP 567
QY 75 LPSEEPSVPADCLEAAQQLNSSLIGCMCHRRMKNQVACLDIYTVHRAARSLGNYELDVS 134
Db 568 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGCFPCP-----VCHSCLSQGREHODGE 623
QY 135 PYEDTVTSKPW--KXNLSKLANMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
Db 624 EFGPGAGSCWCRCQAGQVS-----CVRLQCPPLPKLVQTERGSCPCRCGCLAHG 675
QY 184 E-----ACSGPHCORHVCLRLQLLTFFKAAABPHAGLLCLCP--CAPNDRGCG 228
Db 676 EEHPGSRWVPPDSACSSCVCHGVVTCARIQCISSCAQPR-QG-----PHDCCPQCSDC- 729
QY 229 ERRNTIAPNCALPPVAPNCLLELRRLCFSDP-----LCRSLVDFQTHCHPMDIL-- 278
Db 730 EHEGRKYEPGESFQFGADPC-----EVCICEPQEGPPSLRCHRRQCPSLVGCPPSOLLPP 785
QY 279 -----GTCATEQRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db 786 GPOHCCPTCAEALNSCSE---GLLGSELAP-----PDCYTCQCQDLTWLCTHQACPE 835
QY 326 ECEMLEGFFSHNP-----CLTEATAAKMRHFSQLFSQDWPHTPTFAVMA----- 369
Db 836 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACIACHTCHRG 887
QY 370 ----HONENPAVR--POPW--VPSLFSC 389
Db 888 HVECHLEEQALSCPHGWAKVPOADSC 914
```

RESULT 12

```

US-11-149-003-10
; Sequence 10, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1512
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-11-149-003-10

Query Match          5.9%; Score 129; DB 11; Length 1512;
Best Local Similarity 20.6%; Pred. No. 0.0028;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVHLDSTCTSSISIP 74
DB 678 PDPREPCNLCTCLGGFVTCGRPPGCGSHPLIPSGHCCPTCQGCRCYHGVTTASGETLP 737
QY 75 LPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYVTVHRRARSLGNYELDVS 134
DB 738 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGFCFP-----VCHSCLSQGREHQDGE 793
QY 135 PYEDVTVTSKPM-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
DB 794 ELEGPGAGSCWCRCQAGQVS-----CVRLQCPPLPKLVTERGSCPCRCRGCLAHG 845
QY 184 E-----ACSGPHQCORHVCLRLQLLTFFKAAEPHAGQLLLCP--CAPNDRGCG 228
DB 846 EHEPGSRWVPPDSACSCVCHGVVTCARIQICISSCAQPR-QG-----PHDCCPQSDC- 899
QY 229 ERRRNTIAPNCALPPVAPNCLERLRCFSDP-----LCRSRLVDFQTHCHPMDL-- 278
DB 900 EHEGRKYEPGESFQPGADPC---EVCICEPQEPGPPSLRCHRRQCPSLVGCPPSOLLPP 955
QY 279 -----GTCATEQSRCLRAYLGLIGTAMTFFNVSNVNTSVALSCTCRGSGNL-----Q 325
DB 956 GPQHCCPTCAEALNSCSE---GLLGSELAP-----PDPCYTCQCQDLTLWLCIHQACPE 1005
QY 326 EECMELEGFFSHNP-----CLTEAIAAKMRPHSQLFSQDWHPTFAVMA----- 369
DB 1006 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACTACTCHRG 1057
QY 370 ----HQNENPAVR-POPW--VPSLFSC 389
DB 1058 HVECHLEECQALSCPHGMAKVPQADSC 1084

RESULT 13
US-11-149-003-12
; Sequence 12, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1512
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-11-149-003-12

Query Match          5.9%; Score 129; DB 11; Length 1512;
Best Local Similarity 20.6%; Pred. No. 0.0028;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVHLDSTCTSSISIP 74
DB 678 PDPREPCNLCTCLGGFVTCGRPPGCGSHPLIPSGHCCPTCQGCRCYHGVTTASGETLP 737
QY 75 LPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYVTVHRRARSLGNYELDVS 134
DB 738 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGFCFP-----VCHSCLSQGREHQDGE 793
QY 135 PYEDVTVTSKPM-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
DB 794 ELEGPGAGSCWCRCQAGQVS-----CVRLQCPPLPKLVTERGSCPCRCRGCLAHG 845
QY 184 E-----ACSGPHQCORHVCLRLQLLTFFKAAEPHAGQLLLCP--CAPNDRGCG 228
DB 846 EHEPGSRWVPPDSACSCVCHGVVTCARIQICISSCAQPR-QG-----PHDCCPQSDC- 899
QY 229 ERRRNTIAPNCALPPVAPNCLERLRCFSDP-----LCRSRLVDFQTHCHPMDL-- 278
DB 900 EHEGRKYEPGESFQPGADPC---EVCICEPQEPGPPSLRCHRRQCPSLVGCPPSOLLPP 955
QY 279 -----GTCATEQSRCLRAYLGLIGTAMTFFNVSNVNTSVALSCTCRGSGNL-----Q 325
DB 956 GPQHCCPTCAEALNSCSE---GLLGSELAP-----PDPCYTCQCQDLTLWLCIHQACPE 1005
QY 326 EECMELEGFFSHNP-----CLTEAIAAKMRPHSQLFSQDWHPTFAVMA----- 369
DB 1006 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACTACTCHRG 1057
QY 370 ----HQNENPAVR-POPW--VPSLFSC 389
DB 1058 HVECHLEECQALSCPHGMAKVPQADSC 1084

RESULT 13
US-11-149-003-12
; Sequence 12, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1570
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-11-149-003-12

Query Match          5.9%; Score 129; DB 11; Length 1570;
Best Local Similarity 20.6%; Pred. No. 0.0029;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

QY 33 PLPTESRLMNSCLQ-----ARRKQAD-----PTCSAAVHLDSTCTSSISIP 74
DB 736 PDPREPCNLCTCLGGFVTCGRPPGCGSHPLIPSGHCCPTCQGCRCYHGVTTASGETLP 795
QY 75 LPSEEPSVPADCLEAAQQLRNSLLIGCMCHRRMKNQVACLDIYVTVHRRARSLGNYELDVS 134
DB 796 DPLDPTCSLCTCQEGSMRCQKPCAPALCPHPSPGFCFP-----VCHSCLSQGREHQDGE 851
QY 135 PYEDVTVTSKPM-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
DB 852 ELEGPGAGSCWCRCQAGQVS-----CVRLQCPPLPKLVTERGSCPCRCRGCLAHG 903
QY 184 E-----ACSGPHQCORHVCLRLQLLTFFKAAEPHAGQLLLCP--CAPNDRGCG 228
DB 904 EHEPGSRWVPPDSACSCVCHGVVTCARIQICISSCAQPR-QG-----PHDCCPQSDC- 957
QY 229 ERRRNTIAPNCALPPVAPNCLERLRCFSDP-----LCRSRLVDFQTHCHPMDL-- 278
DB 958 EHEGRKYEPGESFQPGADPC---EVCICEPQEPGPPSLRCHRRQCPSLVGCPPSOLLPP 1013
QY 279 -----GTCATEQSRCLRAYLGLIGTAMTFFNVSNVNTSVALSCTCRGSGNL-----Q 325
DB 1014 GPQHCCPTCAEALNSCSE---GLLGSELAP-----PDPCYTCQCQDLTLWLCIHQACPE 1063
QY 326 EECMELEGFFSHNP-----CLTEAIAAKMRPHSQLFSQDWHPTFAVMA----- 369
DB 1064 LSCPLSE---RHTPPGSCCPVCRECVVEAEGRRV-----ADGESWRDPSNACTACTCHRG 1115
QY 370 ----HQNENPAVR-POPW--VPSLFSC 389
DB 1116 HVECHLEECQALSCPHGMAKVPQADSC 1142

RESULT 14
US-11-149-003-2
; Sequence 2, Application US/11149003
; Publication No. US20060014277A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Kiellin-like Proteins and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/11/149,003
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1570
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-11-149-003-12

```

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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1628
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-149-003-2

Query Match          5.9%; Score 129; DB 11; Length 1628;
Best Local Similarity 20.6%; Pred. No. 0.003;
Matches 92; Conservative 40; Mismatches 185; Indels 130; Gaps 25;

Qy 33 PLPTESLMSCLQ-----ARRKQAD-----PTCSAAVHLDSTSSISTP 74
Db 794 PDPREPCNLCTCLGFGFTTCRRPCEPPGCSHPILIPSGHCCPTCCGCRYHGVTTASGETLP 853
Qy 75 LPSEEPSVPADCLAAQNLNSSLIGCMCHRMKNQVACLDIYVTVHRAISLGNVELDVS 134
Db 854 DPLDPTCSLCTCQSGSMRCQKKPCAPALCPHSPGFCFP-----VCHSCLSQGREHQDGE 909
Qy 135 PYEDTVTSKPW-KMNLKSLKMLKPDSDLCLKF---AMLCTL-----NDKCDRLR--KAYG 183
Db 910 EPEGPAGSCWCRCQAQVS-----CVRLQCPPLPCKLQVTERGCCPCRCGCLAHG 961
Qy 184 E-----ACSGPHCQRHVCLRLQTLTTFEKAABPHAQGLLLCP--CAPNDRGCG 228
Db 962 EEHPGSRWVPPDSACSSCVCHGVVTCARIQCISSCAQPR-QG-----PHDCCPQCSDC- 1015
Qy 229 ERRRTTIAPNCALPPVAPNCLLELRRLCFSDP-----LCRSRLVDFQTHCHPMDIL-- 278
Db 1016 EHEGRKYEGESFQPGADPC-----EVCICEFQPEGPPSLRHRQCPSLVGCPCPSQLLPP 1071
Qy 279 -----GTCATEOSRCLRAYLGLIGTAMTNFVSNVNTSVALSCTCRGSGNL-----Q 325
Db 1072 GPQHCCPTCAEALNSCE--GILGSELAP-----PDCYTCQCOQLTWLCIHQACPE 1121
Qy 326 EECMLEGGFFSHNP-----CLTEAIAAKMRHFSQLFSQDWPHTFAVMA----- 369
Db 1122 LSCPLSE--RHTPPGSCCPVCRVCVEABGRV-----ADGESWRDPNACIACHTCHRG 1173
Qy 370 ----HQNENPAVR-PQPM--VPSLFSC 389
Db 1174 HVECHLECOALSCPHGWAKVPOADSC 1200

RESULT 15
US-11-169-041-131
; Sequence 131, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 131
; LENGTH: 2871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-131

Query Match          5.6%; Score 123.5; DB 11; Length 2871;
Best Local Similarity 19.3%; Pred. No. 0.019;
Matches 84; Conservative 46; Mismatches 131; Indels 175; Gaps 25;

Qy 48 RRCQADPTCSAAHYHLDSTSSISTPLPSEFPSPADCLAAQNLNSSLIG---CMC- 103
```

```
Db 2242 RRNCKDEDECEGKH-----DCTEKQMECKN--LIGTYMCICG 2277
Qy 104 --HRRMKNQVACLD-----IYWTVHRAISLGNVELDVSFYEDTVTSKPKMKNLSKL 152
Db 2278 PGYORPPDGGCVDENECQTKPGICENGRCLNTRGSTCECN---DGFTA----- 2324
Qy 153 NMLKPDSDLCLK---FAMLCCTLNDKC---DRLRKAYGEACS-----GPHCQRHVCL 197
Db 2325 ---SPNQDECLDNREGVCFTFVLQNMCOIGSSNRNPNVTKSECCCGDGRGWGPHCE--ICP 2379
Qy 198 RQLLTFFEKAABPHAQGLL-----LC---PCAPNDRGCGERRRNTIAPNCA 240
Db 2380 FQGTVAFKKLC-PHGRGFTMGADIDECKVIHDVCRNGECV--NDRG---SYHCICKTY 2433
Qy 241 LPV-APNCLLELRRLCFSDP-----LCRSRLVDFQTHCHPMDI-----LGTCAE 284
Db 2434 TPDITGTSVDLNE-CNQAPKPCNFIKNTGEGSYQCSCKGYILQEDGRSCKDLDECATK 2492
Qy 285 QSRCLRAYLGLIG---TAMTPNFVSN-----VNTSVALSCTC 318
Db 2493 QHNCQFLCVNTIGFTCKCPGFTQHTTSCIDNNECTSDINLCGSKGICQNTPGSFTCEC 2552
Qy 319 R-----GSGNLQEBCEML-----EGFFSH-----NPCL 341
Db 2553 QRGFSLDQTSCEDECEGNHRCQHCQNIIGGYRCSQPGYLOHYQWNCVDENECL 2612
Qy 342 TEAIAAKMRHFSOLFS 357
Db 2613 SAHICGGASCHNTLGS 2628
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Search completed: May 12, 2006, 02:16:15
Job time : 21.5734 secs

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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:10:01 ; Search time 33.3739 Seconds
(without alignments)
983.470 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPIUSFILPILQLTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	2	US-09-220-528-64
2	2131	100.0	397	2	US-09-187-906-17
3	2131	100.0	397	2	US-09-489-407-17
4	1774	83.2	346	2	US-09-187-906-15
5	1774	83.2	346	2	US-09-489-407-15
6	1646.5	77.3	400	2	US-09-220-528-63
7	1646.5	77.3	400	2	US-09-187-906-21
8	1646.5	77.3	400	2	US-09-949-016-9079
9	1646.5	77.3	400	2	US-09-489-407-21
10	1386	65.0	315	2	US-09-187-906-19
11	1386	65.0	315	2	US-09-489-407-19
12	577.5	27.1	445	2	US-08-861-990-11
13	577.5	27.1	464	2	US-08-957-063-6
14	577.5	27.1	464	2	US-09-487-685-6
15	577.5	27.1	464	2	US-08-802-805D-6
16	577.5	27.1	464	2	US-08-861-990-2
17	577.5	27.1	464	2	US-09-388-316C-6
18	577.5	27.1	664	2	US-08-957-063-18
19	577.5	27.1	664	2	US-09-487-685-18
20	577.5	27.1	664	2	US-08-802-805D-18
21	577.5	27.1	664	2	US-09-388-316C-18
22	574.5	27.0	464	2	US-09-487-685-3
23	574.5	27.0	464	2	US-09-487-685-3
24	574.5	27.0	464	2	US-08-802-805D-3
25	574.5	27.0	464	2	US-09-187-906-13
26	574.5	27.0	464	2	US-08-861-990-9
27	574.5	27.0	464	2	US-09-388-316C-3

28	574.5	27.0	464	2	US-09-489-407-13	Sequence 13, Appl
29	574.5	27.0	664	2	US-08-957-063-16	Sequence 16, Appl
30	574.5	27.0	664	2	US-09-487-685-16	Sequence 16, Appl
31	574.5	27.0	664	2	US-08-802-805D-16	Sequence 16, Appl
32	574.5	27.0	664	2	US-09-388-316C-16	Sequence 16, Appl
33	515	24.2	460	2	US-08-802-805D-22	Sequence 22, Appl
34	515	24.2	460	2	US-09-187-906-11	Sequence 11, Appl
35	515	24.2	460	2	US-09-489-407-11	Sequence 11, Appl
36	513.5	24.1	463	2	US-08-837-199A-10	Sequence 10, Appl
37	513.5	24.1	463	2	US-08-837-199A-12	Sequence 12, Appl
38	513.5	24.1	465	2	US-08-837-199A-2	Sequence 2, Appli
39	513.5	24.1	465	2	US-08-861-990-8	Sequence 8, Appli
40	513.5	24.1	465	2	US-09-388-316C-22	Sequence 22, Appl
41	512.5	24.0	465	2	US-08-837-199A-6	Sequence 6, Appli
42	505.5	23.7	468	2	US-08-802-805D-21	Sequence 21, Appl
43	505.5	23.7	468	2	US-08-837-199A-4	Sequence 4, Appli
44	505.5	23.7	468	2	US-08-860-370-2	Sequence 2, Appli
45	505.5	23.7	468	2	US-09-187-906-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-220-528-64
; Sequence 64, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Murine
US-09-220-528-64

Query Match	100.0%;	Score 2131;	DB 2;	Length 397;
Best Local Similarity	100.0%;	Pred. No. 2.2e-211;		
Matches	397;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
Qy	1	MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRVNSCTQARKKEANPACKAAVQH	60	
Db	1	MGLSWSPRPPLMLLLVLSLWPLGAGNSLATENRVNSCTQARKKEANPACKAAVQH	60	
Qy	61	LGSCCTSLRPLPLEESAMSDCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWHPA	120	
Db	61	LGSCCTSLRPLPLEESAMSDCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWHPA	120	
Qy	121	RSIGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKFKAMLCTLHDKDRLKAYG	180	
Db	121	RSIGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKFKAMLCTLHDKDRLKAYG	180	
Qy	181	EACSGRCORHCLQAOLRSFFKAAASHAOGLLCCAPEDAGGERRNTIAPSCALPS	240	
Db	181	EACSGRCORHCLQAOLRSFFKAAASHAOGLLCCAPEDAGGERRNTIAPSCALPS	240	
Qy	241	VTNCLDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLGTAMTPN	300	
Db	241	VTNCLDLRSFCRADPLCRSLMDFTQCHPMDILGTCAEQSRCLRAYLGLGTAMTPN	300	
Qy	301	FISKVNTTVALSCTCRSGNQLQDECQLRSFSONPCLVEAIAAKMRFHQLFSQDWADS	360	

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Db 301 FISKVNTTVALSCTCGSNLQDECEQLRSFSQNFCLVEATAAKRFRHQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRLQPRLPILSILPLILLQTLW 397
Db 361 TFSVVOQNSNPALRLQPRLPILSILPLILLQTLW 397

RESULT 2
US-09-187-906-17
; Sequence 17, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-187-906-17

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.2e-211;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSRPPPLMLLLVLSLPLGAGNSLATENRVNSCTQARKKCEANPACKAAYQH 60
Db 1 MGLSWSRPPPLMLLLVLSLPLGAGNSLATENRVNSCTQARKKCEANPACKAAYQH 60
QY 61 LGSCTSSLSRPLPLEESAMSDADCLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHPA 120
Db 61 LGSCTSSLSRPLPLEESAMSDADCLEAAEQLRNSLIDCRCHRRMKHQATCLDIYVTVHPA 120
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QY 121 RSLGDEYLDVSPYEDVTTSKPKMNLKLNMLKPSDILCLKFAMLCCTLHDKCDRLRKAYG 180
Db 121 RSLGDEYLDVSPYEDVTTSKPKMNLKLNMLKPSDILCLKFAMLCCTLHDKCDRLRKAYG 180
QY 181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGGERRENTIAPSCALPS 240
Db 181 EACSGIRCORHLCLAQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGGERRENTIAPSCALPS 240
QY 241 VTPNCLDLRSFCRADPLCRSLRMLDFQTHCHPMIILGTCTATEQSRLRAYLGLIGTAMTNN 300
Db 241 VTPNCLDLRSFCRADPLCRSLRMLDFQTHCHPMIILGTCTATEQSRLRAYLGLIGTAMTNN 300
QY 301 FISKVNTTVALSCTCGSNLQDECEQLRSFSQNPCLVEATAAKRFRHQLFSQDWADS 360
Db 301 FISKVNTTVALSCTCGSNLQDECEQLRSFSQNPCLVEATAAKRFRHQLFSQDWADS 360
QY 361 TFSVVOQNSNPALRLQPRLPILSILPLILLQTLW 397
Db 361 TFSVVOQNSNPALRLQPRLPILSILPLILLQTLW 397

RESULT 3
US-09-489-407-17
; Sequence 17, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-09-489-407-17

Query Match      100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.2e-211;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSWSRPPLMTLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Db 1 MGLSWSRPPLMTLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYQH 60
Qy 61 LGSCTSSLSPLPLEESAMSADCLAAEQLRNSLIIDCRCHRRMKHOATCLDIYVTHPA 120
Db 61 LGSCTSSLSPLPLEESAMSADCLAAEQLRNSLIIDCRCHRRMKHOATCLDIYVTHPA 120
Qy 121 RSLGDIYELDVSPYEDTTSKPKWNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
Db 121 RSLGDIYELDVSPYEDTTSKPKWNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
Qy 181 EACSGIRCORHLCLAQILRSFPEKAAESHAQGLLCPAPEDAGCGERRNTIAPSCALPS 240
Db 181 EACSGIRCORHLCLAQILRSFPEKAAESHAQGLLCPAPEDAGCGERRNTIAPSCALPS 240
Qy 241 VTPNCLDLRSFCRADPLCRSRLMDFOHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
Db 241 VTPNCLDLRSFCRADPLCRSRLMDFOHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPN 300
Qy 301 FISKVNTVALSCTCRSGNLQDECEQLERSFSONPCLVEAIAAKMFHRLQFSQDWADS 360
Db 301 FISKVNTVALSCTCRSGNLQDECEQLERSFSONPCLVEAIAAKMFHRLQFSQDWADS 360
Qy 361 TFSVVOQNSNPALRLQPLPILSILPLILQTLW 397
Db 361 TFSVVOQNSNPALRLQPLPILSILPLILQTLW 397

RESULT 4
US-09-187-906-15
; Sequence 15, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-15

Query Match:      83.2%; Score 1774; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3e-174;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 LSRPLPLEESAMSADCLAAEQLRNSLIIDCRCHRRMKHOATCLDIYVTHPARSLGDYE 127
Db 17 LSRPLPLEESAMSADCLAAEQLRNSLIIDCRCHRRMKHOATCLDIYVTHPARSLGDYE 76
Qy 128 LDVSPYEDTTSKPKWNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGACSGIR 187
Db 77 LDVSPYEDTTSKPKWNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGACSGIR 136
Qy 188 CORHLCLAQILRSFPEKAAESHAQGLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLD 247
Db 137 CORHLCLAQILRSFPEKAAESHAQGLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLD 196
Qy 248 LRSFCRADPLCRSRLMDFOHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFIKVT 307
Db 197 LRSFCRADPLCRSRLMDFOHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFIKVT 256
Qy 308 TVALSCTCRSGNLQDECEQLERSFSONPCLVEAIAAKMFHRLQFSQDWADSTFSVVOQ 367
Db 257 TVALSCTCRSGNLQDECEQLERSFSONPCLVEAIAAKMFHRLQFSQDWADSTFSVVOQ 316
Qy 368 QNSNPALRLQPLPILSILPLILQTLW 397
Db 317 QNSNPALRLQPLPILSILPLILQTLW 346

RESULT 5
US-09-489-407-15
; Sequence 15, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
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; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-489-407-15

Query Match 83.2%; Score 1774; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.3e-174;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	68	LSRPLPLESAMSADCLEAAEQLRNSSLIDCRHRMKHQATCLDIYVTHPARSLGDYE	127
DB	17	LSRPLPLESAMSADCLEAAEQLRNSSLIDCRHRMKHQATCLDIYVTHPARSLGDYE	76
QY	128	LDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCKFAMLTCLDHCRLKAYGEACSGIR	187
DB	77	LDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCKFAMLTCLDHCRLKAYGEACSGIR	136
QY	188	CQRHLCLAQLRSFFKAAESHAQGLLLCPCAPEDAGCGERRNTIAPSCALPSVTNCLD	247
DB	137	CQRHLCLAQLRSFFKAAESHAQGLLLCPCAPEDAGCGERRNTIAPSCALPSVTNCLD	196
QY	248	LSRFCRADPLCRSRLMDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAMTNFISKVNT	307
DB	197	LSRFCRADPLCRSRLMDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAMTNFISKVNT	256
QY	308	TVALSCTCRSGNLODECEQLERSFSONPCLVEAIAAKMFRHQLFSQDWDSTFVSQQ	367
DB	257	TVALSCTCRSGNLODECEQLERSFSONPCLVEAIAAKMFRHQLFSQDWDSTFVSQQ	316
QY	368	QNSNPALRQPLRPILSILPILLLQTLW	397
DB	317	QNSNPALRQPLRPILSILPILLLQTLW	346

RESULT 6
US-09-220-528-63
; Sequence 63, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29

; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-220-528-63

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY	7	PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOHLGSGT	65
DB	9	PLPVPVLMLLLLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAAYHHLDSCT	68
QY	66	SSLSRPLPLESAMSADCLEAAEQLRNSSLIDCRHRMKHQATCLDIYVTHPARSLGD	125
DB	69	SSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYVTHRRARSLGN	128
QY	126	YELDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCKFAMLTCLDHCRLKAYGEACSG	185
DB	129	YELDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCKFAMLTCLDHCRLKAYGEACSG	188
QY	186	IRCQRHLCLAQLRSFFKAAESHAQGLLLCPCAPEDAGCGERRNTIAPSCALPSVTNCP	245
DB	189	PHCQRHVCLRLQLTTFEKAAPHAQGLLLCPCAPNDRCGGERRRNTIAPNCALPPVAPNC	248
QY	246	LDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAMTNFISKV	305
DB	249	LELRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAMTNFVSNV	308
QY	306	NTVALSCTCRSGNLODECEQLERSFSONPCLVEAIAAKMFRHQLFSQDWDSTFVSQ	365
DB	309	NTSVALSCTCRSGNLODECEMLEGFFSHNPCLTEAIAAAMRPHSQLFSQDWPHTFAVM	368
QY	366	QOQNSNPALRQPLRPILSILPILLLQTLW	397
DB	369	AHQENPAVRPQWPVPSLFSCTPLPILLLSLW	400

RESULT 7
US-09-187-906-21
; Sequence 21, Application US/09187906
; Patent No. 6671135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US97/07726
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300

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; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-21

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LIMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYOHLGSC 65
Db 9 PLPPVVLMLLLPLPSPPLAAGDPLPTESELMNSCLQARRKQADPTCSAAVHLLDSC 68
QY 66 SSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYVTVHPARSLG 125
Db 69 SSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMNQVACLDIYVTVHARS LGN 128
QY 126 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 185
Db 129 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 188
QY 186 IRCQRHLCLAQLRSPFEKAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSPVTPNC 245
Db 189 PHCQRHVCLRLQLTFFFEKAEPHAQGLLLCPAPEDAGCGERRRNTIAPNCALPPVAPNC 248
QY 246 LDLSRCPADPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
Db 249 LEURLCFSDPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNV 308
QY 306 NTTVALSCTCRSGNLQDECEQLERSFQNPCLVEAIAAKORFHRQLFSQDWDADSTFSVV 365
Db 309 NTSVALSCTCRSGNLQDECEMLEGFFSHNPCLTEAIAAKORFHSQLFSDQWPHPTFAVM 368
QY 366 OQNSNPALRLOPRLPILSILPLILLQTLW 397
Db 369 AHQENPAVRPQWPVPSLFSCTLPILLILLSLW 400

RESULT 8
US-09-949-016-9079
; Sequence 9079, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9079
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9079

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LIMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAAYOHLGSC 65
Db 9 PLPPVVLMLLLPLPSPPLAAGDPLPTESELMNSCLQARRKQADPTCSAAVHLLDSC 68
QY 66 SSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYVTVHPARSLG 125
Db 69 SSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMNQVACLDIYVTVHARS LGN 128
QY 126 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 185
Db 129 YELDVSPYEDTVTSKPKMNLKLNMLKPDSDILCLKPFAMLC TLHDKCDRLRKAYGEACSG 188
QY 186 IRCQRHLCLAQLRSPFEKAESHAQGLLLCPAPEDAGCGERRRNTIAPSCALPSPVTPNC 245
Db 189 PHCQRHVCLRLQLTFFFEKAEPHAQGLLLCPAPEDAGCGERRRNTIAPNCALPPVAPNC 248
QY 246 LDLSRCPADPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
Db 249 LEURLCFSDPLCRSLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNV 308
QY 306 NTTVALSCTCRSGNLQDECEQLERSFQNPCLVEAIAAKORFHRQLFSQDWDADSTFSVV 365
Db 309 NTSVALSCTCRSGNLQDECEMLEGFFSHNPCLTEAIAAKORFHSQLFSDQWPHPTFAVM 368
QY 366 OQNSNPALRLOPRLPILSILPLILLQTLW 397
Db 369 AHQENPAVRPQWPVPSLFSCTLPILLILLSLW 400

RESULT 9
US-09-489-407-21
; Sequence 21, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-489-407-21

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 2.4e-161;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKEANPACKAAAYQHLGSGCT 65
DB 9 PLPPVVVLMILLPLPPSPLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAHYHLLDST 68

QY 66 SLSRLPLEESAMSDCLEAARQLRNSLIDCRCHRRMKHQATCLDIYTVHPARSLGD 125
DB 69 SSISTPLPEEESPVPADCLEAARQLRNSLIDCRCHRRMKHQATCLDIYTVHPARSLGN 128

QY 126 YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDILCKFAMLCTLHDKDLRLKAYGACSG 185
DB 129 YELDVSPYEDTVTSKPKWNLSKLNMLKPDSDILCKFAMLCTLHDKDLRLKAYGACSG 188

QY 186 IRCORHLCLAQLRSFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNC 245
DB 189 PHCQRHVCLRLQLTFEKAAPHAQGLLLCPAPEDAGCGERRNTIAPSCALPPVAPNC 248

QY 246 LDLRSFCRADPLCRSLMDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKV 305
DB 249 LEHLRLCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSV 308

QY 306 NTTVALSCTCRSGNLQDECEQLERSFSONPCLVEAIAAKMRPHQLFSQDWDADTFSTV 365
DB 309 NTSVALSCTCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRPHSOLFSQDWPHTFAVM 368

QY 366 QOONSNPALRLQPLILSFSILPLILQTLW 397
DB 369 AHQNPENPAVRPQWPVPSLFSCTPLILLLSLW 400

RESULT 10
US-09-187-906-19
; Sequence 19, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM: floppy disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-19

Query Match 65.0%; Score 1386; DB 2; Length 315;
Best Local Similarity 82.2%; Pred. No. 1.4e-134;
Matches 254; Conservative 17; Mismatches 38; Indels 0; Gaps 0;

QY 89 QLRNSSLIDCRCHRRMKHQATCLDIYTVHPARSLGDYELDVSPYEDTVTSKPKWNLSK 148
DB 7 QLRNSSLIGCMCHRRMKHQVACLDIYTVHRRARSLGNLYELDVSPYEDTVTSKPKWNLSK 66

QY 149 LNMKPDSDILCKFAMLCTLHDKDLRLKAYGACSGIRCORHLCLAQLRSFEKAAESH 208
DB 67 LNMKPDSDILCKFAMLCTLHDKDLRLKAYGACSGHQRHVCLRLQLTFEKAAPH 126

QY 209 AQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSLMDFQTH 268
DB 127 AQGLLLCPAPNDRCGERRNTIAPNCALPPVAPNCLRLRCLFSDPLCRSLVDFQTH 186

QY 269 CHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFISKVNTVALSCTCRSGNLQDECEQL 328
DB 187 CHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTVALSCTCRSGNLQEECEML 246

QY 329 ERSFSONPCLVEAIAAKMRPHQLFSQDWDADTFSTVVOONSNPALRLQPLILSFSIL 388
DB 247 EGFFSHNPCLTEAIAAKMRPHSOLFSQDWPHTFAVMAHONENPAVRPQWPVPSLFSCT 306

QY 389 PLILLQTLW 397
DB 307 PLILLLSLW 315

RESULT 11
US-09-489-407-19
; Sequence 19, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21

```

;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Biogen, Inc.
 ; STREET: 14 Cambridge Center
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02142
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/489,407
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/07726
 ; FILING DATE: 07-MAY-97
 ; APPLICATION NUMBER: US 60/017,427
 ; FILING DATE: 08-MAY-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/019,300
 ; FILING DATE: 07-JUN-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/021,859
 ; FILING DATE: 16-JUL-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/043,533
 ; FILING DATE: 10-APR-97
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kaplan, Warren A.
 ; REGISTRATION NUMBER: 34,199
 ; REFERENCE/DOCKET NUMBER: A008 PCT CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-679-2400
 ; TELEFAX: 617-679-2838
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 315 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-489-407-19

Query Match 65.0%; Score 1386; DB 2; Length 315;
 Best Local Similarity 82.2%; Pred. No. 1.4e-134;
 Matches 254; Conservative 17; Mismatches 38; Indels 0; Gaps 0;
 QY 89 QLENSLIDCRHRRMKHQATCLDIYWTVPARSLGDIYELDVSPYEDTTSKPKWKNLSK 148
 DB 7 QLENSLIGCMCHRMKNQVACLDIYTVHRAESLGNLYELDVSPYEDTTSKPKWKNLSK 66
 QY 149 LNMKPDSDLCFKFAMCTLHDKCDRLRKAYGACSGIRQORHLCLAQLRSPFEKAESH 208
 DB 67 LNMKPDSDLCFKFAMCTLHDKCDRLRKAYGACSGPHQORHVCLRLTLTPEKAESH 126
 QY 209 AQGLLCPAPEDAGCGERRRNTIAPSCALPSTPNCLDLRSFCRADPLCRSLMDPOTH 268
 DB 127 AQGLLCPAPEDAGCGERRRNTIAPSCALPSTPNCLDLRSFCRADPLCRSLMDPOTH 186
 QY 269 CHPMIDILGTATQSCRLRAYLGLIGTAMTPNFISKVNTVALSCTCRSGNLDCEQL 328
 DB 187 CHPMIDILGTATQSCRLRAYLGLIGTAMTPNFVSNVNTVALSCTCRSGNLDCEQL 246
 QY 329 ERSFQNPCLVEIAAARPHRLQFSQDWDADSTFVQQQNSNPALRLQPLRPLFSFIL 388
 DB 247 EGFSSHNPCLTEIAAKRHFSLQFSQDWDADSTFVQQQNSNPALRLQPLRPLFSFIL 306
 QY 389 PLILQLTIW 397
 DB 307 PLILLSLW 315

RESULT 12
 US-08-861-990-11
 ; Sequence 11, Application US/08861990
 ; Patent No. 669259
 ; GENERAL INFORMATION:
 ; APPLICANT: Ibanez, Carlos F.
 ; APPLICANT: Arumae, Urmas
 ; APPLICANT: Sariola, Hannu
 ; APPLICANT: Suvarito, Petro
 ; APPLICANT: Trupp, Miles
 ; APPLICANT: Saarna, Mart
 ; TITLE OF INVENTION: Glial Cell Line-Derived Neurotropic Factor Receptors
 ; FILE REFERENCE: CEPH0418
 ; CURRENT APPLICATION NUMBER: US/08/861,990
 ; CURRENT FILING DATE: 1997-05-22
 ; PRIOR APPLICATION NUMBER: 08/747,842
 ; PRIOR FILING DATE: 1996-11-13
 ; PRIOR APPLICATION NUMBER: 60/006,619
 ; PRIOR FILING DATE: 1995-11-13
 ; PRIOR APPLICATION NUMBER: 60/015,767
 ; PRIOR FILING DATE: 1996-04-16
 ; PRIOR APPLICATION NUMBER: 60/021,965
 ; PRIOR FILING DATE: 1996-08-27
 ; PRIOR APPLICATION NUMBER: 60/020,638
 ; PRIOR FILING DATE: 1996-06-27
 ; PRIOR APPLICATION NUMBER: 60/020,639
 ; PRIOR FILING DATE: 1996-06-27
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 ; US-08-861-990-11

Query Match 27.1%; Score 577.5; DB 2; Length 445;
 Best Local Similarity 38.8%; Pred. No. 7.2e-51;
 Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;
 QY 41 CTOARKCEANPACKAAYQHLGSCSTSLRPLLESAMSDCLEAEQRLNSLIDCR 100
 DB 40 CVRANELCAABSNCSRYRTLQCLAGRDNTWL-----ANKCOALEVLQESPLYDCRC 95
 QY 101 HRRMKHQATCLDIYWTVPARSLGDIYELDVSPYEDTTSKPKWKNLSKLNML----- 152
 DB 96 KRGKMKELQCLQIYNSIHGLTEGEFEYASPYE-PVTSR-----LSDIFRLASIFSGTG 149
 QY 153 -----KPDSDLCFKFAMCTLHDKCDRLRKAYGEACS-----GIRQORHLCLAQLRSPFE 202
 DB 150 TDPVSTKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRRKCHKALRQFFD 209
 QY 203 KAASHAQGLLCPAPEDAGCGERRRNTIAPSCAL-PSVTNCLDLRSFCRADPLCRSR 261
 DB 210 RVSEYTYRMLFCSC--QDQACAEERRRQTLPSCYEDKEKPNCLDLRLSLCRTDHLCSR 267
 QY 262 LMDFOQHCHP--MDILGTATQSCRLRAYLGLIGTAMTPNFISKVNTVALS--CTCRG 317
 DB 268 LADFHANCASVYRTTSCPADNYOACLGSTAGMIGDMTPNYVDSPNTGIVVSPWNCRG 327
 QY 318 SGNLQDECEQLRSFSQNFCLVEAIAA 344
 DB 328 SGNMEECEKFLRDFTFENCLRNAIOA 354

RESULT 13
 US-08-957-063-6
 ; Sequence 6, Application US/08957063
 ; Patent No. 6025157
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
 ; TITLE OF INVENTION: Neurturin Receptor
 ; NUMBER OF SEQUENCES: 19

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,063
FILING DATE: 24-Oct-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871
FILING DATE: 9-Jun-1997
PRIOR APPLICATION DATA: 913
APPLICATION NUMBER: 913
FILING DATE: 18-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-957-063-6

Query Match      27.1%; Score 577.5; DB 2; Length 464;
Best Local Similarity 38.8%; Pred. No. 7.6e-51;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;

QY 41 CTQARKKCEANPACAAAYQHLSCTSSLSRPLPLEESAMSDCLEAAEOLRNSSLIDCRC 100
Db 40 CVRANELCAAESNCSSRYRTLQCLAGRDNTML-----ANKCQAALVQLQESPLYDCRC 95

QY 101 HRMKHQATCLDIYTWTHPARSLGDIYELDVSPYEDVTTSKPWKMLSKLNM-----152
Db 96 KRGMKELQCLQIYVSIHLGLTEGEFFYEASPYE-PVTSR-----LSDIFRLASIFSGTG 149

QY 153 -----KPDSDLCLKFAMLTCLHDKDLRKAYGEACS-----GIRQORHLCLAQLRSFPE 202
Db 150 TDPVSTKSNHCLDAKACNLNDNCKLRSYISICNREISPTERCNRKCHKALRQFFD 209

QY 203 KAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSYTYRMLFCS--QDQACAEERRQTILPSCSYEDKEKPNCLDLRLSLCRTDHLCRSR 267

QY 262 LMDPQTHCHP--MDILGTCTATGSCRLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRG 317
Db 268 LADFHANCRASTRYTTSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIWVSPWCNCRG 327

QY 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
Db 328 SGNWEECEKEFLRDFTFENPCLRNAIOA 354

RESULT 14
US-09-487-685-6
; Sequence 6, Application US/09487685
; Patent No. 6342348
; GENERAL INFORMATION:
; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
; TITLE OF INVENTION: Neurturin Receptor
; NUMBER OF SEQUENCES: 19

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/487,685
FILING DATE: 19-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,063
FILING DATE: <Unknown>
APPLICATION NUMBER: 913
FILING DATE: 18-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-487-685-6

Query Match      27.1%; Score 577.5; DB 2; Length 464;
Best Local Similarity 38.8%; Pred. No. 7.6e-51;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;

QY 41 CTQARKKCEANPACAAAYQHLSCTSSLSRPLPLEESAMSDCLEAAEOLRNSSLIDCRC 100
Db 40 CVRANELCAAESNCSSRYRTLQCLAGRDNTML-----ANKCQAALVQLQESPLYDCRC 95

QY 101 HRMKHQATCLDIYTWTHPARSLGDIYELDVSPYEDVTTSKPWKMLSKLNM-----152
Db 96 KRGMKELQCLQIYVSIHLGLTEGEFFYEASPYE-PVTSR-----LSDIFRLASIFSGTG 149

QY 153 -----KPDSDLCLKFAMLTCLHDKDLRKAYGEACS-----GIRQORHLCLAQLRSFPE 202
Db 150 TDPVSTKSNHCLDAKACNLNDNCKLRSYISICNREISPTERCNRKCHKALRQFFD 209

QY 203 KAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
Db 210 RVPSYTYRMLFCS--QDQACAEERRQTILPSCSYEDKEKPNCLDLRLSLCRTDHLCRSR 267

QY 262 LMDPQTHCHP--MDILGTCTATGSCRLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRG 317
Db 268 LADFHANCRASTRYTTSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIWVSPWCNCRG 327

QY 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
Db 328 SGNWEECEKEFLRDFTFENPCLRNAIOA 354

RESULT 15
US-08-802-805D-6
; Sequence 6, Application US/08802805D
; Patent No. 6372453
; GENERAL INFORMATION:
; APPLICANT: Robert D. Klein
; TITLE OF INVENTION: Neurturin Receptor
; NUMBER OF SEQUENCES: 28

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```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,805D
FILING DATE: 18-Feb-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-802-805D-6

Query Match      27.1%; Score 577.5; DB 2; Length 464;
Best Local Similarity 38.8%; Pred. No. 7.6e-51;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;

QY 41 CTOARKKCEANPACKAAYQHLSGTSLSRPPLBESAMSADCLEAAEQLRNSSLIDCRC 100
Db 40 CVRANELCAEBSNCSSRYRTLROCLAGRDRTNWL-----ANKBCQAALVQLQESPLYDCRC 95

QY 101 HRRMKHQATCLDIYTWVHPARSLGDIYELDVSPYEDVTTSKPMKWLKLNML-----152
Db 96 KRGKKELQCLQIYWSIHGLTEGEFFYEASPYE-PVTSR-----LSDIFRLASIESGTG 149

QY 153 -----KPDSDCLKLFAMLTLDKCDRLRKAYGEACS-----GIRCORHLCLAQLRSFFE 202
Db 150 TDPAVSTKGNHCLDAKACNLNDCKLRSSYSICNREISPTERCNRKCKHALRQFFD 209

QY 203 KAAESHAQGLLLCPAPEDAGCGERRNTTAPSCAL-PSVTNCLDIRSECRADPLCRSR 261
Db 210 RVPEYTYRMLFCSC--QDQACAEERRQTILPSCSYEDKEKPNCLDLRLSLCRTDHLCSR 267

QY 262 LMDPQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTFNFTSKVNTTVALS--CTCRG 317
Db 268 LADFHANCRASTYITISCPADNYOACLGSYAGNIGFDMTFNYVDSNPTGIVVSPWCNCRG 327

QY 318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
Db 328 SGNMEECEKFLRDFTEPCLRNAIOA 354

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Search completed: May 12, 2006, 02:11:41
Job time : 34.3739 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 01:59:25 ; Search time 140.527 Seconds
(without alignments)
1250.660 Million cell updates/sec

Title: US-10-668-936-21

Perfect score: 2190

Sequence: 1 MVRPLNRPPLPPVVMLLL.....PWVSLFSCPLPLILLSLW 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	2190	100.0	400	2 AAW37463	AAW37463 Human Ret
3	2190	100.0	400	2 AAW84186	AAW84186 Glial cel
4	2190	100.0	400	3 AAY83226	AAY83226 PRO538 Po
5	2190	100.0	400	3 AAY84590	AAY84590 Amino aci
6	2190	100.0	400	3 AAY15177	AAY15177 Human GFR
7	2190	100.0	400	3 AAB19582	AAB19582 Human PRO
8	2190	100.0	400	3 AAB24411	AAB24411 Human PRO
9	2190	100.0	400	3 AAB00171	AAB00171 PRO538 po
10	2190	100.0	400	3 AAB24050	AAB24050 Human PRO
11	2190	100.0	400	8 ADJ58713	ADJ58713 Human ret
12	2190	100.0	400	8 ADT94302	ADT94302 Human PRO
13	2190	100.0	400	9 ADY53849	ADY53849 Human ret
14	2190	100.0	400	9 ADZ00213	ADZ00213 Human Ret
15	2190	100.0	628	3 AAY15179	AAY15179 GFRalpha3
16	2186	99.8	400	2 AAW84180	AAW84180 A GDNFR-a
17	2184	99.7	400	2 AAW65117	AAW65117 Human GDN
18	2043	93.3	378	2 AAW84185	AAW84185 Glial cel
19	1996.5	91.2	369	3 AAY15178	AAY15178 Human GFR
20	1996.5	91.2	369	3 AAB19583	AAB19583 Human PRO
21	1996.5	91.2	369	3 AAB24051	AAB24051 Human PRO
22	1708	78.0	315	2 AAW37462	AAW37462 Human Ret
23	1708	78.0	315	8 ADJ58711	ADJ58711 Human ret
24	1708	78.0	315	8 ADY53847	ADY53847 Partial h

25	1708	78.0	315	9 ADZ00211	Adz00211 Human Ret
26	1646.5	75.2	397	2 AAW37461	AAW37461 Mouse Ret
27	1646.5	75.2	397	3 AAY84591	Aay84591 Amino aci
28	1646.5	75.2	397	3 AAY15174	Aay15174 Murine GF
29	1646.5	75.2	397	8 ADJ58709	Adj58709 Murine re
30	1646.5	75.2	397	9 ADY53845	Ady53845 Mouse ret
31	1646.5	75.2	397	9 ADZ00209	Adz00209 Mouse Ret
32	1642.5	75.0	397	2 AAW84182	AAW84182 A GDNFR-a
33	1567	71.6	888	3 AAY15182	Aay15182 GD-GFRalp
34	1455	66.4	346	2 AAW37465	AAW37465 Mouse Ret
35	1455	66.4	346	8 ADJ58707	Adj58707 Murine re
36	1455	66.4	346	9 ADY53843	Ady53843 Partial m
37	1455	66.4	346	9 ADZ00207	Adz00207 Mouse Ret
38	1064	48.6	366	9 AEA39229	Aea39229 GRAL-rela
39	944	43.1	172	2 AAW65118	Aaw65118 Human GDN
40	632.5	28.9	498	2 AAW84183	AAW84183 Consensus
41	589.5	26.9	489	2 AAW84298	AAW84298 Consensus
42	547.5	25.0	460	2 AAW84181	AAW84181 A GDNFR-a
43	544.5	24.9	411	2 AAW81625	AAW81625 Mouse mat
44	544.5	24.9	463	2 AAW81624	AAW81624 Mouse TGF
45	543.5	24.8	951	3 AAY15180	Aay15180 GD-GFRalp

ALIGNMENTS

RESULT 1
AAW65116
ID AAW65116 standard; protein; 400 AA.
XX
AC AAW65116;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human GDNF alpha-3 receptor protein #1.
XX
KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
KW muscular dystrophy; diagnostic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..400
FT /label= GDNF alpha-3
FT /note= "Partial sequence"
XX
EP846764-A2.
PD 10-JUN-1998.
XX
PF 20-NOV-1997; 97EP-00309375.
XX
PR 27-NOV-1996; 96GB-00024677.
PR 09-MAY-1997; 97GB-00009463.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Lawrence GMP;
XX
DR WPI; 1998-299980/27.
DR N-PSDB; AAV35364.
XX
PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used
PT to treat neuro degenerative diseases, muscular diseases and nerve and
XX muscle trauma and in diagnostic assays.
XX
PS Claim 4; Fig 2; 22pp; English.
XX
CC This sequence represents a novel glial cell line-derived neurotrophic
CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat

CC e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic
CC lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's
CC Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases
CC (including the muscular dystrophies) and nerve and muscle trauma and in
CC diagnostic assays for such conditions
XX
SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVLMMLLLPSPPLAAGDPLPTESLMNSCLOARRKCOADPTCSAA 60
DB 1 MVRPLNRPPLPPVLMMLLLPSPPLAAGDPLPTESLMNSCLOARRKCOADPTCSAA 60
QY 61 YHLDSTCTSSISTPLPSEPSVPADCLEAAQQLRNSLIGCMCHRRMKQVACLDIYWTV 120
DB 61 YHLDSTCTSSISTPLPSEPSVPADCLEAAQQLRNSLIGCMCHRRMKQVACLDIYWTV 120
QY 121 HRARSLGNVELDVSPEYEDVTTSKPKWKNLSKLNMLKPDSDCLCFAMLTCLNDKCDRLRK 180
DB 121 HRARSLGNVELDVSPEYEDVTTSKPKWKNLSKLNMLKPDSDCLCFAMLTCLNDKCDRLRK 180
QY 181 AYGEACSGPHCRHVCLRQLLTFFEKAAEPHAQGLLCPAPNDRCGRRRTIAPNCA 240
DB 181 AYGEACSGPHCRHVCLRQLLTFFEKAAEPHAQGLLCPAPNDRCGRRRTIAPNCA 240
QY 241 LPPVAPNCLERLRLCFSDPLCRSLRVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
DB 241 LPPVAPNCLERLRLCFSDPLCRSLRVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEIAAKMRFHSQLFSQDW 360
DB 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEIAAKMRFHSQLFSQDW 360
QY 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400
DB 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400

RESULT 2
AAW37463
ID AAW37463 standard; protein; 400 AA.
XX

AC AAW37463;

XX 21-MAY-1998 (first entry)

XX Human Ret ligand RetL3.

XX Ret ligand; RetL3; RetL3; RetL3; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
KW motor neuron disease; multiple sclerosis; infection; meningitis;
KW myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
KW muscular dystrophy; myasthenia gravis; tumour; therapy.

XX Homo sapiens.

XX W09744356-A2.

XX 27-NOV-1997.

XX 07-MAY-1997; 97MO-US007726.

XX 08-MAY-1996; 96US-0017427P.

XX 07-JUN-1996; 96US-0019300P.

XX 16-JUL-1996; 96US-0021859P.

XX 11-APR-1997; 97US-0043533P.

XX (BIOJ) BIOGEN INC.

XX Sanicola-Nadel M, Hession C, Cate RL;
PI WPI; 1998-018431/02.
XX N-PSDB; AAV00251.
XX
PT New nucleic acid encoding ret receptor ligands and related proteins -
PT vectors, transformed cells and antibodies, used for promoting cell growth
PT and improving survival of injured cells, especially renal or nerve cells.
XX
PS Claim 2; Page 85-86; 113pp; English.

XX This amino acid sequence comprises human Ret ligand (RetL) RetL3, deduced
CC from cDNA clones (see AAV00251) isolated from a adult heart and spinal
CC cord libraries. Rat and human RetL1, human RetL2 and mouse RetL3
CC sequences (see AAW37457-62) are also claimed. Human RetL3 is 34.3%
CC identical to human RetL1, 34.9% identical to human RetL2 and 76.8%
CC identical to murine RetL3. Ret ligand is a key component of the Ret
CC signalling pathway that specifically interacts with Ret receptor protein,
CC triggering Ret dimerisation and/or autophosphorylation of the Ret
CC tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic or
CC eukaryotic host cells transformed or transfected with these vectors are
CC claimed, as well as a method for production of RetL3, its soluble
CC variants and fusion proteins with a toxin, imageable compound or
CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
CC used to promote growth of new tissue and survival of damaged tissue.
CC particularly kidney or neural tissue. Typical applications are in renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
CC neurodegeneration, motor neuron disease, multiple sclerosis, bacterial,
CC viral or prion infections (e.g. meningitis, myelopathy associated with
CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC developmental disorders such as Down's syndrome and cerebral palsy, or
CC conditions involving the peripheral nervous system (Lyme disease,
CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
CC deliver toxins etc. to Ret-expressing cells, especially tumours

XX Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVLMMLLLPSPPLAAGDPLPTESLMNSCLOARRKCOADPTCSAA 60
DB 1 MVRPLNRPPLPPVLMMLLLPSPPLAAGDPLPTESLMNSCLOARRKCOADPTCSAA 60
QY 61 YHLDSTCTSSISTPLPSEPSVPADCLEAAQQLRNSLIGCMCHRRMKQVACLDIYWTV 120
DB 61 YHLDSTCTSSISTPLPSEPSVPADCLEAAQQLRNSLIGCMCHRRMKQVACLDIYWTV 120
QY 121 HRARSLGNVELDVSPEYEDVTTSKPKWKNLSKLNMLKPDSDCLCFAMLTCLNDKCDRLRK 180
DB 121 HRARSLGNVELDVSPEYEDVTTSKPKWKNLSKLNMLKPDSDCLCFAMLTCLNDKCDRLRK 180
QY 181 AYGEACSGPHCRHVCLRQLLTFFEKAAEPHAQGLLCPAPNDRCGRRRTIAPNCA 240
DB 181 AYGEACSGPHCRHVCLRQLLTFFEKAAEPHAQGLLCPAPNDRCGRRRTIAPNCA 240
QY 241 LPPVAPNCLERLRLCFSDPLCRSLRVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
DB 241 LPPVAPNCLERLRLCFSDPLCRSLRVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEIAAKMRFHSQLFSQDW 360
DB 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEIAAKMRFHSQLFSQDW 360
QY 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400
DB 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400

RESULT 3
AAW84186


```

FT site
XX WO200021996-A2.
XX 20-APR-2000.
XX 05-OCT-1999; 99WO-US023089.
XX 13-OCT-1998; 98US-0104080P.
XX (GETH ) GENENTECH INC.
XX Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI,
PI Yuan J;
XX WPI; 2000-317943/27.
XX N-PSDB; AA293702.
XX Composition for inhibiting neoplastic cell growth and treating cancers of
PT ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
PT PRO538, PRO172 or PRO182 polypeptide or their agonist.
XX Claim 10; Fig 6; 122pp; English.
XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
CC polypeptide or their agonists, mixed with a carrier is useful for
CC inhibiting neoplastic growth and treating tumors such as cancers of
CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
CC central nervous system, melanoma and leukaemia
XX Sequence 400 AA;
Query Match 100.0%; Score 2190; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVRPLNRPPLPVVLMILLPSPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
DB 1 MVRPLNRPPLPVVLMILLPSPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
QY 61 YHLDSTCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWT 120
DB 61 YHLDSTCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWT 120
QY 121 HRARSLGNYELDVSPYEDTTSKPKWNLKSLNMLKPDSDCLKFMALCTLNDKCDRLK 180
DB 121 HRARSLGNYELDVSPYEDTTSKPKWNLKSLNMLKPDSDCLKFMALCTLNDKCDRLK 180
QY 181 AYGEACGPHCQRHVCLRLQLLTFEKAABPHAQGLLLCPAPNDRGGERRRNTIAPNCA 240
DB 181 AYGEACGPHCQRHVCLRLQLLTFEKAABPHAQGLLLCPAPNDRGGERRRNTIAPNCA 240
QY 241 LPVAPNCLRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAM 300
DB 241 LPVAPNCLRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLGTAM 300
QY 301 TPNFVSNVNTSVALSCTCRSGNMQBCECMLEGGFHSNPNCLTAIAAKMRFHSLQFSQDW 360
DB 301 TPNFVSNVNTSVALSCTCRSGNMQBCECMLEGGFHSNPNCLTAIAAKMRFHSLQFSQDW 360
QY 361 PHPTFAVMQHONENPAVRPQWPVPSLFTPLILLISLW 400
DB 361 PHPTFAVMQHONENPAVRPQWPVPSLFTPLILLISLW 400
RESULT 5
AAV84590
ID AAY84590 standard; protein; 400 AA.
XX AAY84590;
XX 25-JUL-2000 (first entry)
XX

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DE Amino acid sequence of a human growth factor receptor-alpha precursor.
XX Human; artemin; growth factor; neurotrophic factor; trophic support;
KW neuron; trigeminal ganglion neuron; nodose ganglion neuron;
KW superior cervical ganglion neuron; midbrain neuron; Alzheimer's disease;
KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
KW Parkinson's disease; Huntington's disease; acute brain injury;
KW acute spinal cord injury; nervous system tumour; blastoma;
KW multiple sclerosis; infection; enteric disease; idiopathic constipation;
KW Parkinson's disease; small cell lung carcinoma.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..31 /note= "signal peptide"
FT Peptide 32..372
FT Protein /note= "mature protein"
FT Modified-site 95
FT /note= "putative N-linked glycosylation site"
FT Modified-site 148
FT /note= "putative N-linked glycosylation site"
FT Modified-site 309
FT /note= "putative N-linked glycosylation site"
XX WO200018799-A1.
XX 06-APR-2000.
XX 29-SEP-1999; 99WO-US022604.
XX 29-SEP-1998; 98US-00163283.
XX 12-NOV-1998; 98US-0108148P.
XX 22-DEC-1998; 98US-00218698.
XX (UNIW ) UNIV WASHINGTON.
XX Milbrandt JD, Baloh RH;
XX WPI; 2000-293109/25.
XX Isolated artemin growth factor proteins and the nucleic acids that encode
PT them, useful for treating a range of degenerative neuronal disorders such
PT as Parkinson's disease and Huntington's disease.
XX Disclosure; Fig 12; 96pp; English.
XX The present sequence represents a human growth factor receptor-alpha
CC precursor. The specification describes an artemin growth factor protein.
CC Artemin is a neurotrophic factor that belongs to the GDNF (glial cell
CC line-derived neurotrophic factor)/neurturin/persephin family of growth
CC factors and promotes differentiation, maintains mature phenotype and
CC provides trophic support, promoting growth and survival of neurons.
CC Artemin promotes the survival of trigeminal ganglion neurons, nodose
CC ganglion neurons, superior cervical ganglion neurons and tyrosine-
CC hydroxylase-expressing dopaminergic ventral midbrain neurons. Artemin is
CC the only member of the GDNF family that binds to GFR-alpha (growth factor
CC receptor-alpha) and activates the GFR-alpha3/RET (Ret protein-tyrosine
CC kinase) receptor complex and additionally, like GDNF and neurturin,
CC artemin also binds to and activates GFRalpha/RET. Artemin polypeptides
CC and polynucleotides are administered to treat peripheral neuropathy,
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, ischemic stroke, acute brain injury, acute spinal
CC cord injury, a nervous system tumour (e.g. blastoma), multiple
CC sclerosis, infection or enteric disease (e.g. idiopathic constipation or
CC constipation associated with Parkinson's disease, spinal cord injury or
CC use of opiate pain killers). They may also be used to treat a patient
CC suffering from small cell lung carcinoma
XX Sequence 400 AA;
SQ
Query Match 100.0%; Score 2190; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;

```


FT Modified-site 95..99 /note= "Asn is N-glycosylated"

FT Modified-site 148..152 /note= "Asn is N-glycosylated"

FT Modified-site 231..235 /note= "O-phosphorylated"

FT Modified-site 279..285 /note= "N-myristoylation"

FT Modified-site 294..300 /note= "N-myristoylation"

FT Binding-site 306..317 /note= "prokaryotic membrane lipoprotein lipid attachment site"

FT Modified-site 309..313 /note= "Asn is N-glycosylated"

FT Binding-site 379..390 /note= "prokaryotic membrane lipoprotein lipid attachment site"

XX WO200053760-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US006319.

XX 12-MAR-1999; 99US-0123957P.

XX (GETH) GENENTECH INC.

XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ; Kabakoff RC, Klein RD, Kljavin IJ, Kuo SS, La Fleur M, Wood WI; WPI; 2000-587437/55.

XX N-PSDB; AAA88519.

XX Novel PRO polypeptides useful for preventing or rescuing retinal cells from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia, uveitis.

XX Claim 2; Fig 14; 140pp; English.

XX The present sequence is that of human PRO538, as predicted from a cDNA clone (see AAA88519) isolated from a foetal lung tissue cDNA library using probes and primers (see AAA88539-41) based on a cDNA clone isolated from an expressed sequence tag database screening using murine GFR-alpha-3. PRO538 has a predicted mol.wt. of 44,511 and a pI of about 8.15. A splice variant (PRO3664, see AAB19583) of PRO538 was also identified; PRO3664 has a 31-amino acid deletion (amino acid positions 127-157 of PRO538). The invention provides a method for producing PRO polypeptides, including PRO538, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal ganglion cells, amacrine cells, displaced amacrine cells, horizontal and bipolar neurons, and supportive cells (including Mueller cells and pigment epithelial cells) from injury and degradation. The retinal cells are preferably photoreceptors and photoreceptor cell injury or death is caused by retinal injury, light or environmental trauma or by an ocular disease selected from retinitis pigmentosa, macular degeneration, including age-related, retinal detachment, retinal tears, retinopathy, retinal degenerative diseases, macular holes, degenerative myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or contusion such as Purtscher's retinopathy, edema, ischemic conditions such as central or branch retinal vision occlusion, collagen vascular diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and occlusion associated with Eales disease and systemic lupus erythematosus (claimed)

XX Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 3; Length 400;

Best Local Similarity 100.0%; Pred. No. 1.5e-193;

Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVLMILLIPPSPLPLAAGDPLPESRLMNSCLQARRKCOADPTCSAA 60

Db 1 MVRPLNRPPLPPVLMILLIPPSPLPLAAGDPLPESRLMNSCLQARRKCOADPTCSAA 60

QY 61 YHLDSCCTSSISTPLPSEEPSVPADCLAAQQLRNSSLIGCMCHRMKNQVACLDIYWTV 120

Db 61 YHLDSCCTSSISTPLPSEEPSVPADCLAAQQLRNSSLIGCMCHRMKNQVACLDIYWTV 120

QY 121 HPARSIGNVELDVSPYEDTVTSKPWKMLSKLMMKPDSDCLCFAMLCITLNDKCDRLK 180

Db 121 HPARSIGNVELDVSPYEDTVTSKPWKMLSKLMMKPDSDCLCFAMLCITLNDKCDRLK 180

QY 181 AYGEACSGPHCORHVCLQLLTFEKAEPHAQGLLLCPAPNDGCGRRRTNTAPNCA 240

Db 181 AYGEACSGPHCORHVCLQLLTFEKAEPHAQGLLLCPAPNDGCGRRRTNTAPNCA 240

QY 241 LPPVAPNCLLELRRLCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

Db 241 LPPVAPNCLLELRRLCFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

QY 301 TENFVSNVNTSVALSCTCRGSGNLQECCEMLEGFSHPNCLTEATAAKMRFHSQSFQDW 360

Db 301 TENFVSNVNTSVALSCTCRGSGNLQECCEMLEGFSHPNCLTEATAAKMRFHSQSFQDW 360

QY 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400

Db 361 PHPTFAVMAHQENPAVRPQWPVPSLFCSTLPLILLLSLW 400

RESULT 8

AAB24411

ID AAB24411 standard; protein; 400 AA.

XX AC AAB24411;

XX 07-NOV-2000 (first entry)

XX Human PRO538 protein sequence SEQ ID NO:132.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; cytoatonic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytoatonic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1998; 98WO-US025108.

XX 16-DEC-1998; 98US-0112850P.

XX 12-JAN-1999; 99US-0115554P.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-OCT-1999; 99US-0162506P.

XX (GETH) GENENTECH INC.

PA

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
 PI Smith V, Watanabe CK, Williams PM, Wood WI;
 XX WPI; 2000-412154/35.
 DR N-PSDB; AAA77617.
 XX
 XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 PT and treating diagnosing a cardiovascular, endothelial or angiogenic
 PT disorders in mammals.
 XX
 XX Claim 72; Fig 48; 315pp; English.
 XX
 XX The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the prevention,
 CC treatment and diagnosis of diseases associated with inappropriate PRO
 CC expression such as cardiovascular, endothelial or angiogenic disorders in
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
 CC example, the nucleic acids (NCs) and vectors containing them and the PRO
 CC polypeptide may be used to treat disorders associated with decreased PRO
 CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
 CC nucleotide and protein sequences used in the exemplification of the
 CC present invention
 XX
 XX Sequence 400 AA;
 SQ
 Query Match 100.0%; Score 2190; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVRPLNRPPLPPVVMMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVVMMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
 QY 61 YHLDSTCTSSITPLPSEEPSVPADCLAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTV 120
 DB 61 YHLDSTCTSSITPLPSEEPSVPADCLAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTV 120
 QY 121 HRARSLGNYELDVSPYEDTTSKPKWKNLSKLNKLPDSDCLCKFAMLCITLNDKCDRLK 180
 DB 121 HRARSLGNYELDVSPYEDTTSKPKWKNLSKLNKLPDSDCLCKFAMLCITLNDKCDRLK 180
 QY 181 AYGEACSGPHCQHVCLRLQLLTTFEKAABPHAOGLLLCPCAPNDRGCGRRRNTIAPNCA 240
 DB 181 AYGEACSGPHCQHVCLRLQLLTTFEKAABPHAOGLLLCPCAPNDRGCGRRRNTIAPNCA 240
 QY 241 LPPVAPNCLERLRCFSDPLCRSLRVDPFQTHCPMDILGTCATEQSRCLRAYLGLGTAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLRVDPFQTHCPMDILGTCATEQSRCLRAYLGLGTAM 300
 QY 301 TPNFVSNVNTSVALSCTCRSGNMQECEMLEGFFSHNPCLTEAIAAKMRFHQLFSQDW 360
 DB 301 TPNFVSNVNTSVALSCTCRSGNMQECEMLEGFFSHNPCLTEAIAAKMRFHQLFSQDW 360
 QY 361 PHTFVMAHQNENPAVRPQWPVPSLPSCTPLILLLSLW 400
 DB 361 PHTFVMAHQNENPAVRPQWPVPSLPSCTPLILLLSLW 400
 RESULT 9
 AAB00171
 ID AAB00171 standard; protein; 400 AA.
 XX
 AC AAB00171;
 XX
 XX 08-FEB-2001 (first entry)
 DT
 XX PRO538 polypeptide.

XX PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour;
 KW treatment; agonist; antibody; breast cancer; ovarian cancer;
 KW renal cancer; colorectal cancer; uterine cancer; prostate cancer;
 KW lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder;
 KW angiogenic disorder; immunologic disorder; human.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 PH Peptide 1..26
 FT /label= Signal peptide
 FT Modified-site 95..99
 FT /note= "N-glycosylation site"
 FT Modified-site 134..138
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 148..152
 FT /note= "N-glycosylation site"
 FT Modified-site 170..174
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 202..206
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 231..235
 FT /note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 279..285
 FT /note= "N-myristoylation site"
 FT Modified-site 294..300
 FT /note= "N-glycosylation site"
 FT Binding-site 306..317
 FT /label= Prokaryotic membrane lipoprotein lipid attachment site
 FT Modified-site 309..313
 FT /note= "N-glycosylation site"
 FT Domain 379..395
 FT /label= Transmembrane domain
 FT Binding-site 379..390
 FT /label= Prokaryotic membrane lipoprotein lipid attachment site
 XX WO200055319-A1.
 PN 21-SEP-2000.
 PD
 XX 02-DEC-1999; 99WO-US028564.
 XX
 XX 12-MAR-1999; 99US-0123957P.
 PR 28-APR-1999; 99US-0131445P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 05-OCT-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
 PI Yuan J;
 XX
 XX WPI; 2000-638201/61.
 DR N-PSDB; AAA54101.
 XX
 XX PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for
 PT treating tumors including cancers of the breast and lung, leukemia and
 PT for identifying compounds capable of inhibiting growth of neoplastic
 PT cells.
 XX
 XX Claim 31; Fig 6; 133pp; English.
 PS
 XX Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their
 CC agonists (preferably anti-PRO agonist antibody or a small molecule
 CC mimicking the biological activity of PRO polypeptide) are useful in vitro

or in vivo for inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic cell growth and for treating cancer including breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, central nervous system cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, blastocoeleic disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO polypeptides by contacting the polypeptide with a candidate molecule and monitoring biological activity mediated by the polypeptide

XX Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
 DB 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60

QY 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120
 DB 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120

QY 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180
 DB 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180

QY 181 AYGEACSGPHCORHVCLRLQLTFEKAAPHAQGLLLCPAPNDRCGGRRNTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLRLQLTFEKAAPHAQGLLLCPAPNDRCGGRRNTIAPNCA 240

QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

QY 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEAIAAKRFRHSQLSQDW 360
 DB 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEAIAAKRFRHSQLSQDW 360

QY 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400
 DB 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400

RESULT 10

ID AAB24050 standard; protein; 400 AA.

XX AAB24050;

XX 25-JAN-2001 (first entry)

XX Human PRO538 protein sequence SEQ ID NO:20.

XX Human; tumour; diagnosis; neoplastic disease; identification; cancer;
 XX tumorigenesis; detection; neoplastic cell growth; proliferation;
 XX cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
 XX immunological disorder.

XX Homo sapiens.

XX WO200053754-A1.

XX 14-SEP-2000.

XX 06-JAN-2000; 2000WO-US000277.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 05-OCT-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;
 XX Wood WI;
 PI WPI; 2000-572269/53.
 DR N-PSDB; AAC58234.
 XX New isolated antibody for use in compositions and methods for the
 PT diagnosis and treatment of neoplastic cell growth and proliferation in
 PT mammals, including humans, and in monitoring tumor treatment.
 XX Claim 61; Fig 20; 195pp; English.

XX The present invention describes an isolated antibody (Ab) that binds to
 CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
 CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO538, PRO3664, PRO618,
 CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions and
 CC methods for the diagnosis and treatment of neoplastic cell growth and
 CC proliferation in mammals, including humans. Genes and polypeptides
 CC be identified and are useful targets for the treatment and prevention of
 CC certain cancers and may be used to monitor tumor treatment. Compounds
 CC that inhibit the expression or activity of the identified polypeptides
 CC can be identified and used as antagonists. Benign or malignant tumours,
 CC inflammatory disorders and immunological disorders can be treated.
 CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
 CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
 CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention

XX Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
 DB 1 MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60

QY 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120
 DB 61 YHLDSCSTSSISTPLPSPSPVPADCLEAAQQLRNSLLIGCMCHRRMKQVACLDIYWTV 120

QY 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180
 DB 121 HRARSLGNELVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLKPFAMLTCLNDKCDRLRK 180

QY 181 AYGEACSGPHCORHVCLRLQLTFEKAAPHAQGLLLCPAPNDRCGGRRNTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLRLQLTFEKAAPHAQGLLLCPAPNDRCGGRRNTIAPNCA 240

QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAM 300

QY 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEAIAAKRFRHSQLSQDW 360
 DB 301 TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPFCLTEAIAAKRFRHSQLSQDW 360

QY 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400
 DB 361 PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLLSLW 400

```

RESULT 11
ADJ58713
ID ADJ58713 standard; protein; 400 AA.
XX
AC ADJ58713;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human retL3 protein.
XX
KW Tissue growth; retL protein; organ failure; foetal malformation;
KW tumour growth; renal tissue; cytostatic; vulnery; nephrotropic; human.
XX
OS Homo sapiens.
XX
PN US6677135-B1.
XX
PD 13-JAN-2004.
XX
PF 06-NOV-1998; 98US-00187906.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US007726.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
WPI: 2004-079845/08.
DR N-PSDB; ADJ58712.
XX
New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
PT treating diseases or conditions associated with aberrant expression or
PT activity of the Ret ligand, such as organ failure, fetal malformations
PT and tumor growth.
XX
PS Claim 1; SEQ ID NO 21; 66pp; English.
XX
CC The present invention relates to nucleotide and amino acid sequences
CC which promote tissue growth and methods for modulating tissue growth. The
CC invention also relates to retL proteins and polynucleotides encoding such
CC proteins. RetL proteins interact with a receptor protein Ret to trigger
CC dimerisation and/or autophosphorylation of the tyrosine kinase domain of
CC the receptor protein Ret. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of diseases or
CC conditions associated with aberrant expression or activity of the Ret
CC ligand, such as organ failure, foetal malformations and tumour growth and
CC for promoting regeneration or survival of damaged renal tissue. The
CC present sequence is human retL3 protein of the invention.
XX
SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 8; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNRPPLPPVLMMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCCQADPTCSAA 60
DB 1 MVRPLNRPPLPPVLMMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCCQADPTCSAA 60
QY 61 YHHLDSCTSSITPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTY 120
DB 61 YHHLDSCTSSITPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTY 120
QY 121 HRARSLGNLYDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCKFAMLTCLNDKCDRLRK 180
DB 121 HRARSLGNLYDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCKFAMLTCLNDKCDRLRK 180

181 AYGEACSGPHCQRHVCLRQLLTFFEKAAEPHAQGLLPCAPNDRGCGERRNTIAPNCA 240
181 AYGEACSGPHCQRHVCLRQLLTFFEKAAEPHAQGLLPCAPNDRGCGERRNTIAPNCA 240
241 LPPVAPNCLRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
241 LPPVAPNCLRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
301 TPNFVSNVNTSVALSCTCRSGNQLQECCEMLEGFFSHNPCLTETAIARAKMRFHLSQSDW 360
301 TPNFVSNVNTSVALSCTCRSGNQLQECCEMLEGFFSHNPCLTETAIARAKMRFHLSQSDW 360
361 PHPTFAVMAHQENPAVRPQWPVPSLFSCTPLILLLSLW 400
361 PHPTFAVMAHQENPAVRPQWPVPSLFSCTPLILLLSLW 400

RESULT 12
ADT94302
ID ADT94302 standard; protein; 400 AA.
XX
AC ADT94302;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human PRO538 protein.
XX
KW cytostatic; ophthalmological; cardiant; vulnery; angiogenesis inhibitor;
KW angiogenesis stimulator; cardiovascular; gene therapy; diagnosis;
KW mutation; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; myocardial infarction; cardiac hypertrophy; trauma;
KW cancer; macular degeneration; PGF2alpha; primary angioplasty.
XX
OS Homo sapiens.
XX
PN AU2003259607-A1.
XX
PD 27-NOV-2003.
XX
PF 31-OCT-2003; 2003AU-00259607.
XX
PR 30-NOV-1999; 2000AU-00017482.
XX
(GETH ) GENENTECH INC.
XX
PI Williams PM, Watanabe CK, Smith V, Paoni NF, Kuo SS, Klein RD;
PI Gurney AL, Godowski PJ, Goddard A, Hillan KJ, Gerber H, Ferrara N;
PI Baker KP, Ashkenazi AJ, Wood WI;
XX
WPI: 2004-662630/65.
DR N-PSDB; ADT94301.
XX
Diagnosing disease e.g. cardiovascular, endothelial or angiogenic
PT disorder in mammal, related to mutation in PRO1303 polypeptide-encoding
PT nucleic acid sequence, by determining presence or absence of mutation in
PT nucleic acid sequence.
XX
Example 27; SEQ ID NO 132; 301pp; English.
XX
The invention relates to a method of diagnosing (M1) a disease or
CC susceptibility to a disease which is related to a mutation in a PRO1303
CC polypeptide-encoding nucleic acid sequence, by determining the presence
CC or absence of the mutation in the polypeptide-encoding nucleic acid
CC sequence, where the presence or absence of the mutation is indicative of
CC the presence or absence of the disease or susceptibility to the disease.
CC The method is useful for diagnosing a disease or susceptibility to a
CC disease e.g. cardiovascular, endothelial or angiogenic disorder in a
CC mammal. The method is also useful for treating a cardiovascular,
CC endothelial or angiogenic disorder in a mammal, especially human. The
CC human has suffered myocardial infarction. The human has cardiac
CC hypertrophy, trauma, a cancer or age-related macular degeneration. The
CC cardiac hypertrophy is characterized by the presence of an elevated level

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CC of PGF2alpha. The PRO1303 polypeptide is administered together with a
 CC cardiovascular, endothelial or angiogenic agent. The PRO-1303 polypeptide
 CC is administered following primary angioplasty. The cardiovascular,
 CC endothelial or angiogenic disorder is cancer. The method is useful for
 CC inhibiting endothelial cell growth in a mammal. The method is further
 CC useful for stimulating endothelial cell growth in a mammal. The PRO1303
 CC nucleic acid molecule or polypeptide is useful in the manufacture of a
 CC medicament for treating or diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder in a mammal. The medicament is for treating humans.
 CC This sequence corresponds to a PRO protein of the invention.

XX Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 8; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNPRPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
 DB 1 MVRPLNPRPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
 QY 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSLLIGCMCHRMKNQVACLDIYWTV 120
 DB 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSLLIGCMCHRMKNQVACLDIYWTV 120
 QY 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLK 180
 DB 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLK 180
 QY 181 AYGEACSGPHCORHVCLRLQLTFFPKAAEPHQAQGLLLCPCAPNDRCGERRNTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLRLQLTFFPKAAEPHQAQGLLLCPCAPNDRCGERRNTIAPNCA 240
 QY 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRLCLAYLGLIGTAM 300
 DB 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRLCLAYLGLIGTAM 300
 QY 301 TENFVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPFCLTEATAAKMRFHSOLFSDW 360
 DB 301 TENFVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPFCLTEATAAKMRFHSOLFSDW 360
 QY 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400
 DB 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400

RESULT 13
 ADY53849
 ID ADY53849 standard; protein; 400 AA.

XX ADY53849;
 AC ADY53849;

XX 05-MAY-2005 (first entry)
 DT Human retL3 protein.

XX DNA purification; immune stimulation; ret ligand.
 KW Homo sapiens.

XX US6861509-B1.
 PN 01-MAR-2005.

XX 21-JAN-2000; 2000US-00489407.
 XX 08-MAY-1996; 96US-0017427P.

XX 07-JUN-1996; 96US-0019300P.
 XX 16-JUL-1996; 96US-0021859P.

XX 23-AUG-1996; 96US-0023444P.
 XX 11-APR-1997; 97US-0043533P.

XX 07-MAY-1997; 97WO-US007726.
 XX 06-NOV-1998; 98US-00187906.

XX (BIOJ) BIOGEN INC.

XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;

XX WPI; 2005-201184/21.
 XX N-PSDB; ADY53848.

XX New anti-Ret ligand (RetL) antibody, useful for treating acute renal
 PT failure, acute nephritis, chronic renal failure, nephrotic syndrome, as
 PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.

XX Disclosure; SEQ ID NO 21; 66pp; English.

XX The invention relates to an antibody produced by a hybridoma selected
 CC from the group consisting of AA.F99 and AA.GE7.3. The antibody is used to
 CC stimulate neural and renal cell growth. This sequence corresponds to a
 CC protein sequence of the invention.

XX Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 9; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.5e-193;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLNPRPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60
 DB 1 MVRPLNPRPLPVVLMMLLLPPSPPLAAGDPLPTESLMNSCLQARRKCOADPTCSAA 60

QY 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSLLIGCMCHRMKNQVACLDIYWTV 120
 DB 61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQQLRNSLLIGCMCHRMKNQVACLDIYWTV 120

QY 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLK 180
 DB 121 HRARSLGNVELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCKFAMLCCTLNDKCDRLK 180

QY 181 AYGEACSGPHCORHVCLRLQLTFFPKAAEPHQAQGLLLCPCAPNDRCGERRNTIAPNCA 240
 DB 181 AYGEACSGPHCORHVCLRLQLTFFPKAAEPHQAQGLLLCPCAPNDRCGERRNTIAPNCA 240

QY 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRLCLAYLGLIGTAM 300
 DB 241 LPPVAPNCLRLRCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRLCLAYLGLIGTAM 300

QY 301 TENFVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPFCLTEATAAKMRFHSOLFSDW 360
 DB 301 TENFVSNVNTSVALSCTCRGSGNLQECMELEGFFSHNPFCLTEATAAKMRFHSOLFSDW 360

QY 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400
 DB 361 PHPTFAVMAHONENPAVRPQWPVPSLFCSTLPLILLLSLW 400

RESULT 14
 ADZ00213
 ID ADZ00213 standard; protein; 400 AA.

XX ADZ00213;
 AC ADZ00213;

XX 30-JUN-2005 (first entry)
 DT Human Ret ligand 3 (RetL3), SEQ ID NO:21.

XX Cell growth; development; signal transduction; neurological disease;
 KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
 KW cancer; neoplasm; cytostatic; RetL3;
 KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
 KW GDNF family receptor alpha 3; GFR3.

XX Homo sapiens.
 XX US2005080235-A1.

XX PD 14-APR-2005.
XX PF 23-SEP-2003; 2003US-00668936.
XX PR 08-MAY-1996; 96US-0017427P.
XX PR 07-JUN-1996; 96US-0019300P.
XX PR 16-JUL-1996; 96US-0021859P.
XX PR 23-AUG-1996; 96US-0023444P.
XX PR 11-APR-1997; 97US-0043533P.
XX PR 07-MAY-1997; 97MO-US007726.
XX PR 06-NOV-1998; 98US-00187906.
XX (SANI/) SANICOLA-NADEL M.
PA (HESS/) HESSION C.
PA (CATE/) CATE R L.
PA (WORL/) WORLEY D S.
XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX WPI; 2005-305025/31.
XX N-PSDB; AD200212.
XX
XX New polypeptide sequence that interacts with a receptor protein Ret to
XX trigger dimerization or autophosphorylation, useful in preparing a
XX composition for treating neurodegenerative disorders, e.g., Alzheimer's
XX disease.
XX
XX Claim 1; SEQ ID NO 21; 67pp; English.
XX
XX The invention relates to the murine and human RetL3 (Ret ligand 3)
XX proteins (AD200209 and AD200213, respectively) and to proteins at least
XX 80% identical to murine or human RetL3. The invention also discloses
XX other RetL3 proteins such as rat RetL1, human RetL1, human RetL2,
XX fragments of human RetL1, mouse RetL3, and human RetL3, and cDNA sequences
XX encoding these RetL3 proteins or protein fragments. Like other RetL
XX proteins, the RetL3 proteins of the invention interact with the Ret
XX receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
XX triggering Ret receptor dimerization or autophosphorylation. The Ret
XX receptor is expressed during development in a variety of tissues,
XX including the peripheral and central nervous systems and the kidney. It
XX is also expressed in some cancers. RetL3 proteins such as the murine and
XX human RetL3 proteins, and RetL polynucleotides may be used for
XX stimulating Ret receptor signaling, thereby promoting renal or neuronal
XX cell growth or survival and minimizing damage to such tissues after
XX various insults. They may therefore be used to treat renal disorders
XX (e.g., renal failure, renal tube defects and renal trauma) or
XX neurological disorders including neurodegenerative disorders (e.g.,
XX Alzheimer's disease), bacterial or viral diseases of the nervous system
XX (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
XX or trauma) and developmental neural disorders (e.g., mental retardation).
XX Conversely, antibodies against RetL3 may be used to block RetL3-Ret
XX receptor signal transduction for inhibiting tumor growth, fusion proteins
XX comprising a RetL3 protein are useful for targeting a drug to Ret receptor
XX -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
XX also be used in medical imaging. The present sequence represents a
XX specifically claimed full-length human RetL3 protein encoded by cDNA
XX isolated in the invention.
XX
XX SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 9; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-193;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVRPLNRPPLPPVVMULLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
Db 1 MVRPLNRPPLPPVVMULLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA 60
Qy 61 YHLDSCSTSSITPLPSEPSVPADCLAAQQLNSSLIGCMCHRRMNQVACLDIYWTY 120
Db 61 YHLDSCSTSSITPLPSEPSVPADCLAAQQLNSSLIGCMCHRRMNQVACLDIYWTY 120

Qy 121 HRARSLGNVELDVSPYEDTIVTSKPKWNLKSLNMLKPDSDLCKFAMLCITLNDKCDRLRK 180
Db 121 HRARSLGNVELDVSPYEDTIVTSKPKWNLKSLNMLKPDSDLCKFAMLCITLNDKCDRLRK 180
Qy 181 AYGEACSGPHCORHVCLRQLLTFFEKAAEPHAQGLLILCPAPNDRGCGERRNTIAPNCA 240
Db 181 AYGEACSGPHCORHVCLRQLLTFFEKAAEPHAQGLLILCPAPNDRGCGERRNTIAPNCA 240
Qy 241 LPPVAPNCLERLRLCFSDPLCRSLRVLDFQTHCHPMDILGTCAEQSCLRAYLGLIGTAM 300
Db 241 LPPVAPNCLERLRLCFSDPLCRSLRVLDFQTHCHPMDILGTCAEQSCLRAYLGLIGTAM 300
Qy 301 TPNFVSNVNTSVALSCTCRSGNLQEBCEMLEGFFSHNPCLTEAIAAAMRPHSOLFQSDW 360
Db 301 TPNFVSNVNTSVALSCTCRSGNLQEBCEMLEGFFSHNPCLTEAIAAAMRPHSOLFQSDW 360
Qy 361 PHPTFAVMAHONENPAVRPQWPVPSLPSCTPLILLISLW 400
Db 361 PHPTFAVMAHONENPAVRPQWPVPSLPSCTPLILLISLW 400

RESULT 15
AAY15179
ID AAY15179 standard; protein; 628 AA.
XX
XX AC AAY15179;
XX
XX DT 07-FEB-2000 (first entry)
XX
XX DE GFRalpha3-IgG fusion protein.
XX
XX KW GFRalpha3-IgG fusion protein; recombinant expression; epitope tag;
XX Baculovirus-infected insect cell; Baculovirus expression vector;
XX restriction enzyme; subcloning; GFRalpha3 ligand; GFRalpha3;
XX glial-cell-line-derived neurotrophic factor family receptor alpha-3;
XX peripheral nervous system disease; autonomic nervous system dysfunction.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PN WO9949039-A2.
XX
XX PD 30-SEP-1999.
XX
XX PF 19-MAR-1999; 99WO-US006098.
XX
XX PR 23-MAR-1998; 98US-0079124P.
XX PR 13-APR-1998; 98US-0081569P.
XX
XX (GETH) GENENTECH INC.
XX
XX PI De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
XX
XX DR WPI; 2000-038358/03.
XX
XX PT New isolated GFR-alpha3 nucleic acid, used to develop products for
XX treating diseases or conditions involving peripheral nervous system or
XX autonomic nervous system.
XX
XX PS Example 8; Page 101-104; 112pp; English.
XX
XX The present sequence is GFRalpha3-IgG fusion protein. This was used for
XX recombinant expression of GFRalpha3 in Baculovirus-infected insect cells.
XX The GFRalpha3 was fused upstream of an epitope tag contained within a
XX Baculovirus expression vector. The product was digested with selected
XX restriction enzymes and subcloned into the expression vector. This fusion
XX was also used to determine GFRalpha3 binding. GFRalpha3
XX ligands can be useful in the treatment of peripheral nervous system
XX diseases and autonomic nervous system dysfunctions
XX
XX SQ Sequence 628 AA;

Query Match 100.0%; Score 2190; DB 3; Length 628;

Best Local Similarity 100.0%; Pred. No. 2.7e-193;				
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA	60	
Db	1	MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAA	60	
Qy	61	YHLDSTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRMKNQVACLDIYWTV	120	
Db	61	YHLDSTSSISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRMKNQVACLDIYWTV	120	
Qy	121	HRARSLGNVELDVSPYEDVTTSKPMXNLSKLNMLKXPDSDLCIKFAMLCTLNDKCDRLRK	180	
Db	121	HRARSLGNVELDVSPYEDVTTSKPMXNLSKLNMLKXPDSDLCIKFAMLCTLNDKCDRLRK	180	
Qy	181	AYGEACSGPHCQHVCLRQLLTFFEKABPHAQGLLLCPCAPNDRGCGERRNTIAPNCA	240	
Db	181	AYGEACSGPHCQHVCLRQLLTFFEKABPHAQGLLLCPCAPNDRGCGERRNTIAPNCA	240	
Qy	241	LPPVAPNCLERLRCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCRLAYLGLIGTAM	300	
Db	241	LPPVAPNCLERLRCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCRLAYLGLIGTAM	300	
Qy	301	TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEAIAAKMRFHSQLFSDQW	360	
Db	301	TPNFVSNVNTSVALSCTCRSGNLQECMELEGFFSHNPCLTEAIAAKMRFHSQLFSDQW	360	
Qy	361	PHPTFAVMAHQENPAVRQPWPVPSLFSCTPLILLLSLW	400	
Db	361	PHPTFAVMAHQENPAVRQPWPVPSLFSCTPLILLLSLW	400	

Search completed: May 12, 2006, 02:04:18
Job time : 145.527 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 12, 2006, 02:10:01 ; Search time 33.6261 Seconds
(without alignments)
983.470 Million cell updates/sec

Title: US-10-668-936-21
Perfect score: 2190
Sequence: 1 MVRPLNRPPLPPVLMMLL.....PWVPSLFCSTPLILLISLW 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfilesi.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2190	100.0	400	2	US-09-220-528-63
2	2190	100.0	400	2	US-09-187-906-21
3	2190	100.0	400	2	US-09-949-016-9079
4	2190	100.0	400	2	US-09-489-407-21
5	1708	78.0	315	2	US-09-187-906-19
6	1708	78.0	315	2	US-09-489-407-19
7	1646.5	75.2	397	2	US-09-220-528-64
8	1646.5	75.2	397	2	US-09-187-906-17
9	1646.5	75.2	397	2	US-09-489-407-17
10	1455	66.4	346	2	US-09-187-906-15
11	1455	66.4	346	2	US-09-489-407-15
12	542.5	24.8	445	2	US-08-861-990-11
13	542.5	24.8	464	2	US-08-957-063-6
14	542.5	24.8	464	2	US-09-487-685-6
15	542.5	24.8	464	2	US-08-802-805D-6
16	542.5	24.8	464	2	US-08-861-990-2
17	542.5	24.8	464	2	US-09-388-316C-6
18	542.5	24.8	664	2	US-08-957-063-18
19	542.5	24.8	664	2	US-09-487-685-18
20	542.5	24.8	664	2	US-08-802-805D-18
21	542.5	24.8	664	2	US-09-388-316C-18
22	540.5	24.7	464	2	US-08-957-063-3
23	540.5	24.7	464	2	US-09-487-685-3
24	540.5	24.7	464	2	US-08-802-805D-3
25	540.5	24.7	464	2	US-09-187-906-13
26	540.5	24.7	464	2	US-08-861-990-9
27	540.5	24.7	464	2	US-09-388-316C-3

28	540.5	24.7	464	2	US-09-489-407-13	Sequence 13, Appl
29	540.5	24.7	664	2	US-08-957-063-16	Sequence 16, Appl
30	540.5	24.7	664	2	US-09-487-685-16	Sequence 16, Appl
31	540.5	24.7	664	2	US-08-802-805D-16	Sequence 16, Appl
32	540.5	24.7	664	2	US-09-388-316C-16	Sequence 16, Appl
33	517.5	23.6	460	2	US-08-802-805D-22	Sequence 22, Appl
34	517.5	23.6	460	2	US-09-489-407-11	Sequence 11, Appl
35	517.5	23.6	460	2	US-09-187-906-11	Sequence 11, Appl
36	516	23.6	463	2	US-08-837-199A-10	Sequence 10, Appl
37	516	23.6	463	2	US-08-837-199A-12	Sequence 12, Appl
38	516	23.6	465	2	US-08-837-199A-2	Sequence 2, Appl
39	516	23.6	465	2	US-08-861-990-8	Sequence 8, Appl
40	516	23.6	465	2	US-09-388-316C-22	Sequence 22, Appl
41	515	23.5	465	2	US-08-837-199A-6	Sequence 6, Appl
42	511	23.3	468	2	US-08-802-805D-21	Sequence 21, Appl
43	511	23.3	468	2	US-08-837-199A-4	Sequence 4, Appl
44	511	23.3	468	2	US-08-860-370-2	Sequence 2, Appl
45	511	23.3	468	2	US-09-187-906-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-220-528-63
; Sequence 63, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 63
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-63

Query Match 100.0%; Score 2190; DB 2; Length 400;					
Best Local Similarity 100.0%; Pred. No. 4.6e-207;					
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60		
Db	1	MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60		
QY	61	YHLDSCSTSSITPLPSEEPSVPADCLEAAQQLRNSLLGCMCHRMKNQVACLDIYWTV	120		
Db	61	YHLDSCSTSSITPLPSEEPSVPADCLEAAQQLRNSLLGCMCHRMKNQVACLDIYWTV	120		
QY	121	HRARSLGNVELDVSPYEDVTVTSKPMQNLKSNMLKPDSDCLKFMALCTLNDCDRLRK	180		
Db	121	HRARSLGNVELDVSPYEDVTVTSKPMQNLKSNMLKPDSDCLKFMALCTLNDCDRLRK	180		
QY	181	AYGEACSGPHCHVCLRLQLLTFFEKAAEPHAGLLCPCAPNDRCGGERRTIAPNCA	240		
Db	181	AYGEACSGPHCHVCLRLQLLTFFEKAAEPHAGLLCPCAPNDRCGGERRTIAPNCA	240		
QY	241	LPPVAENCLERRLCFSDPLCRSLVDFTQCHPMDILGTCAEQSLRAYLGLGTAM	300		
Db	241	LPPVAENCLERRLCFSDPLCRSLVDFTQCHPMDILGTCAEQSLRAYLGLGTAM	300		
QY	301	TPNFVSNVNTSVALSCTCRSGNLQBECEMLEGFFSHNFCPLTEAIAAKRHFHSQFSDW	360		

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Db      301  TPNFVSNVNTSVALSCTCGSGNLQBECEMLGFFSHNFCPLTEATAAKRPHSOLFSDW 360
      361  PHPTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400
      361  PHPTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400

RESULT 2
US-09-187-906-21
; Sequence 21, Application US/09187906
; Patent No. 667135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-187-906-21

Query Match      100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.6e-207;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
Db      1  MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
QY      61  YHLDSCSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
Db      61  YHLDSCSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
QY      121 HRASLIGNVELDVSPYEDTIVTSKPMKMLSKLNMKPDSDCLCKFAMLCTLNDKCDRLRK 180
Db      121 HRASLIGNVELDVSPYEDTIVTSKPMKMLSKLNMKPDSDCLCKFAMLCTLNDKCDRLRK 180
QY      181 AYGEACSGPHCORHVCLRQLLTFFFEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA 240
Db      181 AYGEACSGPHCORHVCLRQLLTFFFEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA 240
QY      241 LPPVAPNCLLELRRLCFSDPLCRSLRVDFTQTHCPMDILGTCAEQSRCLRAYLIGLIGTAM 300
Db      241 LPPVAPNCLLELRRLCFSDPLCRSLRVDFTQTHCPMDILGTCAEQSRCLRAYLIGLIGTAM 300
QY      301 TPNFVSNVNTSVALSCTCGSGNLQBECEMLGFFSHNFCPLTEATAAKRPHSOLFSDW 360
Db      301 TPNFVSNVNTSVALSCTCGSGNLQBECEMLGFFSHNFCPLTEATAAKRPHSOLFSDW 360
QY      361 PHPTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400
Db      361 PHPTFAVMAHQENPAVRPQPWPVPSLFSCTPLPILLLSLW 400

RESULT 3
US-09-949-016-9079
; Sequence 9079, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9079
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9079

Query Match      100.0%; Score 2190; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.6e-207;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
Db      1  MVRPLNRPPLPPVVLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
QY      61  YHLDSCSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
Db      61  YHLDSCSTSSISTPLPSEEPSVPADCLEAAQQLRNSLIGCMCHRRMKNQVACLDIYWTV 120
QY      121 HRASLIGNVELDVSPYEDTIVTSKPMKMLSKLNMKPDSDCLCKFAMLCTLNDKCDRLRK 180
Db      121 HRASLIGNVELDVSPYEDTIVTSKPMKMLSKLNMKPDSDCLCKFAMLCTLNDKCDRLRK 180
QY      181 AYGEACSGPHCORHVCLRQLLTFFFEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA 240
Db      181 AYGEACSGPHCORHVCLRQLLTFFFEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCA 240
QY      241 LPPVAPNCLLELRRLCFSDPLCRSLRVDFTQTHCPMDILGTCAEQSRCLRAYLIGLIGTAM 300
Db      241 LPPVAPNCLLELRRLCFSDPLCRSLRVDFTQTHCPMDILGTCAEQSRCLRAYLIGLIGTAM 300
QY      301 TPNFVSNVNTSVALSCTCGSGNLQBECEMLGFFSHNFCPLTEATAAKRPHSOLFSDW 360

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Db 301 TPNFVNVNTSVALSCTCRSGNLOECEMELGFFSHNPCLTEAIAAKMRFHSLQFSQDW 360
 Qy 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400
 Db 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400

RESULT 4

US-09-489-407-21

; Sequence 21, Application US/09489407

; Patent No. 6861509

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural

; OPERATING SYSTEM: PC-DOS/MS-DOS

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Biogen, Inc.

; STREET: 14 Cambridge Center

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02142

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/489,407

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/07726

; FILING DATE: 07-MAY-97

; APPLICATION NUMBER: US 60/017,427

; FILING DATE: 08-MAY-96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/019,300

; FILING DATE: 07-JUN-96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/021,859

; FILING DATE: 16-JUL-96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/043,533

; FILING DATE: 10-APR-97

; ATTORNEY/AGENT INFORMATION:

; NAME: Kaplan, Warren A.

; REGISTRATION NUMBER: 34,199

; REFERENCE/DOCKET NUMBER: A008 PCT CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-679-2400

; TELEFAX: 617-679-2838

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 400 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-489-407-21

Query Match

Best Local Similarity 100.0%; Score 2190; DB 2; Length 400;

Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVRPLNRPPLPPVVMILLPLPSPLPLAAGDPLPESRLMNSCLQARRKQADPTCSAA 60

Db 1 MVRPLNRPPLPPVVMILLPLPSPLPLAAGDPLPESRLMNSCLQARRKQADPTCSAA 60

Qy 61 YHLDSCSTSSISPLPSEEPSVPADCLAAQQLRNSLIGCMCHRRMKNQVACLDIYWTY 120

Db 61 YHLDSCSTSSISPLPSEEPSVPADCLAAQQLRNSLIGCMCHRRMKNQVACLDIYWTY 120

Qy 121 HRARSLGNVELDVPYEDTIVTSKPKMNLKLNMLKPDSDLCLKFAMLCFLNDKCDRLRK 180
 Db 121 HRARSLGNVELDVPYEDTIVTSKPKMNLKLNMLKPDSDLCLKFAMLCFLNDKCDRLRK 180
 Qy 181 AYGEACSGPHCORHVCLRLITTFEKAABPHAOGLLLCPCAPNDRGCGERRNTIAPNCA 240
 Db 181 AYGEACSGPHCORHVCLRLITTFEKAABPHAOGLLLCPCAPNDRGCGERRNTIAPNCA 240
 Qy 241 LPPVAPNCLRLCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 Db 241 LPPVAPNCLRLCLFSDPLCRSLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 Qy 301 TPNFVNVNTSVALSCTCRSGNLOECEMELGFFSHNPCLTEAIAAKMRFHSLQFSQDW 360
 Db 301 TPNFVNVNTSVALSCTCRSGNLOECEMELGFFSHNPCLTEAIAAKMRFHSLQFSQDW 360
 Qy 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400
 Db 361 PHPTFAVMAHONENPAVRPQPWVPSLFSCTPLILLISLW 400

RESULT 5

US-09-187-906-19

; Sequence 19, Application US/09187906

; Patent No. 6677135

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Biogen, Inc.

; STREET: 14 Cambridge Center

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02142

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/187,906

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/07726

; FILING DATE: 07-MAY-97

; APPLICATION NUMBER: US 60/017,427

; FILING DATE: 08-MAY-96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/019,300

; FILING DATE: 07-JUN-96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/021,859

; FILING DATE: 16-JUL-96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/043,533

; FILING DATE: 10-APR-97

; ATTORNEY/AGENT INFORMATION:

; NAME: Kaplan, Warren A.

; REGISTRATION NUMBER: 34,199

; REFERENCE/DOCKET NUMBER: A008 PCT CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-679-2400

; TELEFAX: 617-679-2838

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 315 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-187-906-19

Query Match 78.0%; Score 1708; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 9.3e-160;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNLYELDVSPYEDTTSKPWNLSK 151
DB 7 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNLYELDVSPYEDTTSKPWNLSK 66
QY 152 LNMKPDSDCLCKFAMLTCLNDKCDRLRKAYGACSGPHQCORHVCLRLQLLTFEKAAPH 211
DB 67 LNMKPDSDCLCKFAMLTCLNDKCDRLRKAYGACSGPHQCORHVCLRLQLLTFEKAAPH 126
QY 212 AQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDVDFQTH 271
DB 127 AQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDVDFQTH 186
QY 272 CHPMDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALSCTCRSGNLQEECEML 331
DB 187 CHPMDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALSCTCRSGNLQEECEML 246
QY 332 EGFSSHNPCLTEAIAAKRHFHLSOLFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 391
DB 247 EGFSSHNPCLTEAIAAKRHFHLSOLFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 306
QY 392 PLILLLSLW 400
DB 307 PLILLLSLW 315

RESULT 6

US-09-489-407-19
Sequence 19, Application US/09489407
Patent No. 6861509
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
TITLE OF INVENTION: and Renal Growth
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,407
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
PRIOR APPLICATION DATA: US 60/019,300
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
PRIOR APPLICATION DATA: US 60/043,533
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199

REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-489-407-19

Query Match 78.0%; Score 1708; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 9.3e-160;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNLYELDVSPYEDTTSKPWNLSK 151
DB 7 QLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGNLYELDVSPYEDTTSKPWNLSK 66
QY 152 LNMKPDSDCLCKFAMLTCLNDKCDRLRKAYGACSGPHQCORHVCLRLQLLTFEKAAPH 211
DB 67 LNMKPDSDCLCKFAMLTCLNDKCDRLRKAYGACSGPHQCORHVCLRLQLLTFEKAAPH 126
QY 212 AQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDVDFQTH 271
DB 127 AQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLRLCFSDPLCRSLVDVDFQTH 186
QY 272 CHPMDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALSCTCRSGNLQEECEML 331
DB 187 CHPMDILGTCAEQSRCLRAYLGLIGTAMTNPVSNVNTSVALSCTCRSGNLQEECEML 246
QY 332 EGFSSHNPCLTEAIAAKRHFHLSOLFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 391
DB 247 EGFSSHNPCLTEAIAAKRHFHLSOLFSDQWPHPTFAVMAHONENPAVRPOPWVPSLFSCTL 306
QY 392 PLILLLSLW 400
DB 307 PLILLLSLW 315

RESULT 7

US-09-220-528-64
Sequence 64, Application US/09220528A
Patent No. 6284540
GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey D.
TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
FILE REFERENCE: 6029-7998
CURRENT APPLICATION NUMBER: US/09/220,528A
CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 60/108,148
EARLIER FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 64
LENGTH: 397
TYPE: PPT
ORGANISM: Murine
US-09-220-528-64

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 1.5e-153;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
QY 9 PLPPVVMLLLLPSPFLAAGDPLPTESLMNSCLQARRKCOADPTCSAYHLDSC 68
DB 7 PRPP-LLMILLVLSLWFLGAGNSLATENRFVNSCTQARKKEANPACKAAVOHLSCT 65

Qy 69 SSISTPLPSEPSVPADCLEAAQRLNSSLLGCMCHRMKNQVACLDIYTVTHRARSIGN 128
Db 66 SLSRPLPLEBSAMSADCLEAAEQRLNSSLLDCHRRMKHQATCLDIYTVTHRARSIGD 125
Qy 129 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCFAMLTCLNDKCDRLKAYGEACSG 188
Db 126 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCFAMLTCLNDKCDRLKAYGEACSG 185
Qy 189 PHCORHVCRLQLTFFEKAAEPHAQGLLLCPANDRGCGERRNTIAPNCALPPVAPNC 248
Db 186 IRCORHCLLAQLRSFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNC 245
Qy 249 LELRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTFNFSV 308
Db 246 LDLRSFCRADPLCRSRLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTFNFSKV 305
Qy 309 NTSVALSCTCRGSGNLQCECEMLEGFFSHNPLCTEATAAKMRFHSQLFSQDWPHTPVM 368
Db 306 NTTVALSCTCRGSGNLQCECEQLERSFSONPCLVEAIAAKMRFHSQLFSQDWDSTFSV 365
Qy 369 AHONENPAVRPQWPVPSLFSCTPLILLLSLW 400
Db 366 QQNSNPALRLQPLPILSILPLILLQTLW 397

RESULT 8

US-09-187-906-17
; Sequence 17, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-17

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 1.5e-153;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

Qy 9 PLPVPVLMILLPLPPSPPLAAGDPLPESRLMNSCLQARRKQADPTCSAAVHHLDSCT 68
Db 7 PRPP-LIMILLVLSLWPLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAVQHLGSGCT 65
Qy 69 SSISTPLPSEPSVPADCLEAAQRLNSSLLGCMCHRMKNQVACLDIYTVTHRARSIGN 128
Db 66 SLSRPLPLEBSAMSADCLEAAEQRLNSSLLDCHRRMKHQATCLDIYTVTHRARSIGD 125
Qy 129 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCFAMLTCLNDKCDRLKAYGEACSG 188
Db 126 YELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLCFAMLTCLNDKCDRLKAYGEACSG 185
Qy 189 PHCORHVCRLQLTFFEKAAEPHAQGLLLCPANDRGCGERRNTIAPNCALPPVAPNC 248
Db 186 IRCORHCLLAQLRSFFEKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNC 245
Qy 249 LELRLCFSDPLCRSRLVDFQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTFNFSV 308
Db 246 LDLRSFCRADPLCRSRLMDPQTHCHPMDILGTCAEQSRCLRAYLGLIGTAMTFNFSKV 305
Qy 309 NTSVALSCTCRGSGNLQCECEMLEGFFSHNPLCTEATAAKMRFHSQLFSQDWPHTPVM 368
Db 306 NTTVALSCTCRGSGNLQCECEQLERSFSONPCLVEAIAAKMRFHSQLFSQDWDSTFSV 365
Qy 369 AHONENPAVRPQWPVPSLFSCTPLILLLSLW 400
Db 366 QQNSNPALRLQPLPILSILPLILLQTLW 397

RESULT 9
US-09-489-407-17
; Sequence 17, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96

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; PRIOR APPLICATION DATA: US 60/021,859
; APPLICATION NUMBER: 16-JUL-96
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-489-407-17

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 1.5e-153;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 9 PLPPVLMILLPLPPPLAAGDPLPESRLMNSCLQARRKCOADPTCSAAVHLDSC 68
DB 7 PRPP-LLMILLVLSLWLPAGNSLATENRFYNSCTQARKCEANPACKAAVQHIGSCT 65

QY 69 SSTSTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRMKNQVACLDIYVTVHARSIGN 128
DB 66 SLSRPLPSEASMSADCLEAAQQLRNSSLIDCRCHRMKHQATCLDIYVTVHARSIGD 125

QY 129 YELDVSPYEDVTSTKPMKNLSKLNMLKPDSDLCCLKFAMLCCLNDKCDRLRKAYGEACSG 188
DB 126 YELDVSPYEDVTSTKPMKNLSKLNMLKPDSDLCCLKFAMLCCLNDKCDRLRKAYGEACSG 185

QY 189 PHCORHVLRLQTLFFKAAEPHAQGLLLCPAPNDRGCGERRNTIAPNCALPPVAPNC 248
DB 186 IRCORHLCLAQLRSFFKAAESHAQGLLLCPAPNDRGCGERRNTIAPNCALPPVTPNC 245

QY 249 LEIRLFCSDPLCRSLRVDFTQCHPMDILGTCTEQSRCLRAYLGLIGTAMTPNFVSNV 308
DB 246 LDLSRCPADPLCRSLRMDFTQCHPMDILGTCTEQSRCLRAYLGLIGTAMTPNFISKV 305

QY 309 NTSVALSCTCRSGNLOECEMLEGFFSHNPCLTEAIAAKMRPHSQLSQDWPHTFVAVM 368
DB 306 NTVVALSCTCRSGNLOECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDSTFSVV 365

QY 369 AHQENPAVRPQWPVPSLFSCTPLILLSLW 400
DB 366 QQNSNPALRLQRLPLILSPSILPLLILLQTLW 397

RESULT 10
US-09-187-906-15
; Sequence 15, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/187,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-187-906-15

Query Match 66.4%; Score 1455; DB 2; Length 346;
Best Local Similarity 80.9%; Pred. No. 8.6e-135;
Matches 267; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 71 ISTPLPSEPSVPADCLEAAQQLRNSSLIGCMCHRMKNQVACLDIYVTVHARSIGNYE 130
DB 17 LSRPLPSEASMSADCLEAAQQLRNSSLIDCRCHRMKHQATCLDIYVTVHARSIGDYE 76

QY 131 LDVSPYEDVTSTKPMKNLSKLNMLKPDSDLCCLKFAMLCCLNDKCDRLRKAYGEACSGPH 190
DB 77 LDVSPYEDVTSTKPMKNLSKLNMLKPDSDLCCLKFAMLCCLNDKCDRLRKAYGEACSGIR 136

QY 191 CORHVLRLQTLFFKAAEPHAQGLLLCPAPNDRGCGERRNTIAPNCALPPVAPNCLE 250
DB 137 CORHLCLAQLRSFFKAAESHAQGLLLCPAPNDRGCGERRNTIAPNCALPSVTPNCILD 196

QY 251 LRRLFCSDPLCRSLRVDFTQCHPMDILGTCTEQSRCLRAYLGLIGTAMTPNFVSNVT 310
DB 197 LRSFCRADPLCRSLRMDFTQCHPMDILGTCTEQSRCLRAYLGLIGTAMTPNFISKVT 256

QY 311 SVALSCTCRSGNLOECEMLEGFFSHNPCLTEAIAAKMRPHSQLSQDWPHTFVAVMAH 370
DB 257 TVALSCTCRSGNLOECEQLERSFSQNPCLVEAIAAKMRPHRQLFSQDWDSTFSVVOQ 316

QY 371 QNENPAVRPQWPVPSLFSCTPLILLSLW 400
DB 317 QNSNPALRLQRLPLILSPSILPLLILLQTLW 346

RESULT 11
US-09-489-407-15
; Sequence 15, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
```

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Biogen, Inc.
 ; STREET: 14 Cambridge Center
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02142
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/489,407
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA: PCT/US97/07726
 ; FILING DATE: 07-MAY-97
 ; APPLICATION NUMBER: US 60/017,427
 ; FILING DATE: 08-MAY-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/019,300
 ; FILING DATE: 07-JUN-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/021,859
 ; FILING DATE: 16-JUL-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/043,533
 ; FILING DATE: 10-APR-97
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kaplan, Warren A.
 ; REGISTRATION NUMBER: 34,199
 ; REFERENCE/DOCKET NUMBER: A008 PCT CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-679-2400
 ; TELEFAX: 617-679-2838
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-489-407-15

Query Match 66.4%; Score 1455; DB 2; Length 346;
 Best Local Similarity 80.9%; Pred. No. 8.6e-135;
 Matches 267; Conservative 21; Mismatches 42; Indels 0; Gaps 0;
 Qy 71 ISTPLPSEPSVPADCLAEAAQLRNSLLIGCMCHRRMKNQVACLDIYVTVHRAARSLGNYE 130
 Db 17 LSRPLPLESAMSADCLAEAAQLRNSLLIDCRCHRRMKHQATCLDIYVTVHRAARSLGNYE 76
 Qy 131 LDVSPYEDTTSKPKWKNLKLNLKPDSDLCCLKFAMLCNTLNKCDRLRKAYGEACSGPH 190
 Db 77 LDVSPYEDTTSKPKWKNLKLNLKPDSDLCCLKFAMLCNTLNKCDRLRKAYGEACSGIR 136
 Qy 191 CORHVCLRLQLLTPEKAAEHAQGLLILCPAPNDRCGERRNTIAPNCALPPVAPNCL 250
 Db 137 CORHLCUARSPEKAAEHAQGLLILCPAPNDRCGERRNTIAPNCALPPVAPNCL 196
 Qy 251 LRRLCFSDPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNT 310
 Db 197 LRSPCRADPLCRSLVDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNT 256
 Qy 311 SVALSCTCRSGNLOECCEMLEGFFSHNPCLTEIAAANKRPHSOLFQSDWPHPTFAVMAH 370
 Db 257 TVALSCTCRSGNLOECCEQLERSFSQNPCLVEIAAANKRPHRQLFSQDWDSTFVSVOQ 316
 Qy 371 QNENPAVRPOPWPSLFSCTLPILILSLW 400
 Db 317 QNSNPAURLQPRFILSILPLILQLTLW 346

RESULT 12
 US-08-861-990-11
 ; Sequence 11, Application US/08861990
 ; Patent No. 6696259
 ; GENERAL INFORMATION:
 ; APPLICANT: Ibanez, Carlos F.
 ; APPLICANT: Arumae, Urmas
 ; APPLICANT: Sariola, Hannu
 ; APPLICANT: Suvalto, Petro
 ; APPLICANT: Trupp, Miles
 ; APPLICANT: Saarna, Mart
 ; TITLE OF INVENTION: Glial Cell Line-Derived Neurotropic Factor Receptors
 ; FILE REFERENCE: CEPH0418
 ; CURRENT APPLICATION NUMBER: US/08/861,990
 ; CURRENT FILING DATE: 1997-05-22
 ; PRIOR APPLICATION NUMBER: 08/747,842
 ; PRIOR FILING DATE: 1996-11-13
 ; PRIOR APPLICATION NUMBER: 60/006,619
 ; PRIOR FILING DATE: 1995-11-13
 ; PRIOR APPLICATION NUMBER: 60/015,767
 ; PRIOR FILING DATE: 1996-04-16
 ; PRIOR APPLICATION NUMBER: 60/021,965
 ; PRIOR FILING DATE: 1996-06-27
 ; PRIOR APPLICATION NUMBER: 60/020,638
 ; PRIOR FILING DATE: 1996-06-27
 ; PRIOR APPLICATION NUMBER: 60/020,639
 ; PRIOR FILING DATE: 1996-06-27
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 ; US-08-861-990-11
 Query Match 24.8%; Score 542.5; DB 2; Length 445;
 Best Local Similarity 37.4%; Pred. No. 8.2e-45;
 Matches 123; Conservative 42; Mismatches 125; Indels 39; Gaps 10;
 Qy 44 CLQARRKCOADPTCSAAVHHLSDCTS--SISTPLPSEPSVPADCLAEAAQLRNSLLIGC 101
 Db 40 CVRANELCAESNCSSRYRTLRQCLAGDRNTWLANKE-----CQAALEVLQESPLYDC 93
 Qy 102 MCHRRMKNQVACLDIYVTVHRAARSLGNYELDVSPYEDTTSKPKWKNLKLNLML----- 155
 Db 94 RCKRGMKKEIQCLQIYWSIHGLGTEGEFEVASEPYE-PVTSR-----LSDIFRLASIFSG 147
 Qy 156 -----KPDSDLCCLKFAMLCNTLNKCDRLRKAYGEACS-----GPHCQRHVCLRLQLTTF 203
 Db 148 TGTDPAPVSTKSNHCLDAKACACNLNDNCKLRSSYISICNREISPTERCNRRKCKHAKRQF 207
 Qy 204 FEKAAEHAQGLLILCPAPNDRCGERRNTIAPNCAL-PPVAPNCLLERLCFSDPLCR 262
 Db 208 FDRVPSEYTYRMFLFCS--ODQACERRRQTILPSCSYEDKEKPNCLDLRLSCLRTDHLCR 265
 Qy 263 SRLVDFTQCHP--MDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTSVALS--CTC 318
 Db 266 SRLADFHANCASRYRTITPCPADNYOACLSGYAGMIGFDMTPNYVDSNPTGIVVSPWCNC 325
 Qy 319 RGSNGNLOECCEMLEGFFSHNPCLTEIAIA 347
 Db 326 RGSNGNMEEBCEKPLRDTFTENPCLRNAIOA 354

RESULT 13
 US-08-957-063-6
 ; Sequence 6, Application US/08957063
 ; Patent No. 6025157
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
 ; TITLE OF INVENTION: Neurturin Receptor
 ; NUMBER OF SEQUENCES: 19


```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPacIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,805D
; FILING DATE: 18-Feb-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-802-805D-6
;
; Query Match 24.8%; Score 542.5; DB 2; Length 464;
; Best Local Similarity 37.4%; Pred. No. 8.7e-45;
; Matches 123; Conservative 42; Mismatches 125; Indels 39; Gaps 10;
;
; QY 44 CLOARRKCOADPTCSAAYHHLDSCTS--SISTPLPSEEPSVPADCLEAAQQLRNSHLGC 101
; DB 40 CVRANELCAAESNCSSRYTRLQCLAGRDRTMLANKE-----CQAALVLOESPLYDC 93
;
; QY 102 MCHRRMKNOVACLDIYVTVHRARSLGNYELDVSPYEDTVTSKPKMNLKLNML----- 155
; DB 94 RCRGKMKELQCLQIYWSIHLGLTEGEFEYEAAPYE-PVTISR-----LSDIFPLASIFSG 147
;
; QY 156 -----KPDSDLCLKFAMLCITLNDKCDRLRKAYGEACS-----GPHCQRHVCLRLQLTF 203
; DB 148 TGTDPVAVSTKSNHCLDAAKACNLNDCKLRSSYSICNREISPTERCNRRKCKKALRQF 207
;
; QY 204 FEKAAEPHAQGLLLCPAFNDRGCGERRRNTIAPNCAL-PPVAPNCLRLRCLCFSDPLCR 262
; DB 208 FDRVPSEYTYRMLFCSC--QDQACAEERRQTILFSCSYEDKPKENCLDLRLSLCRTDHLCR 265
;
; QY 263 SRLVDFQTHCHP--MDILGTCAEQSRCLRAYLGLIGTAMTPNFVSNVNTSVALS--CTC 318
; DB 266 SRLADFHANCRAHYRITSCPADNYQACLSYAGMIGFDMTPNYVDNPTGIUVSPWCNC 325
;
; QY 319 RGSNGTQEECEMLEGFFSHNPCLTEIAA 347
; DB 326 RGSNGMEECCKFLRDPFENPCLRNAIQA 354

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Search completed: May 12, 2006, 02:11:40
Job time : 36.6261 secs

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OM protein - protein search, using sw model

Run on: May 12, 2006, 01:59:25 ; Search time 139.473 Seconds
(without alignments)
1250.660 Million cell updates/sec

Title: US-10-668-936-17
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLMLLLVLS.....PRLPILSFLPLILLQLTLW 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	397	2 AAW37461	Aaw37461 Mouse Ret
2	2131	100.0	397	3 AAY84591	Aay84591 Amino aci
3	2131	100.0	397	3 AAY15174	Aay15174 Murine GF
4	2131	100.0	397	8 ADJ58709	Adj58709 Murine re
5	2131	100.0	397	9 ADY33845	Ady33845 Mouse ret
6	2131	100.0	397	9 ADZ00209	Adz00209 Mouse Ret
7	1972	92.5	337	2 AAW84182	Aaw84182 A GDNFR-a
8	1880	88.2	888	3 AAY15182	Aay15182 gd-GFRalp
9	1774	83.2	346	2 AAW37465	Aaw37465 Mouse Ret
10	1774	83.2	346	8 ADJ58707	Adj58707 Murine re
11	1774	83.2	346	8 ADY33843	Ady33843 Partial m
12	1774	83.2	346	9 ADZ00207	Adz00207 Mouse Ret
13	1646.5	77.3	400	2 AAW65116	Aaw65116 Human GDN
14	1646.5	77.3	400	2 AAW37463	Aaw37463 Human Ret
15	1646.5	77.3	400	2 AAW84186	Aaw84186 Glial cel
16	1646.5	77.3	400	2 AAY83226	Aay83226 PRO538 Po
17	1646.5	77.3	400	3 AAY84590	Aay84590 Amino aci
18	1646.5	77.3	400	3 AAY15177	Aay15177 Human GFR
19	1646.5	77.3	400	3 AAB19582	Aab19582 Human PRO
20	1646.5	77.3	400	3 AAB24411	Aab24411 Human PRO
21	1646.5	77.3	400	3 AAB00171	Aab00171 PRO538 po
22	1646.5	77.3	400	3 AAB24050	Aab24050 Human PRO
23	1646.5	77.3	400	8 AAB258713	Aab258713 Human ret
24	1646.5	77.3	400	8 ADT94302	Adt94302 Human PRO

25	1646.5	77.3	400	9 ADY53849	Ady53849 Human ret
26	1646.5	77.3	400	9 ADZ00213	Adz00213 Human Ret
27	1646.5	77.3	628	3 AAY15179	Aay15179 GFRalapha3
28	1642.5	77.1	400	2 AAW84180	Aaw84180 A GDNFR-a
29	1640.5	77.0	400	2 AAW85117	Aaw85117 Human GDN
30	1531.5	71.9	378	2 AAW84185	Aaw84185 Glial cel
31	1458	68.4	369	3 AAY15178	Aay15178 Human GFR
32	1458	68.4	369	3 AAB19583	Aab19583 Human PRO
33	1458	68.4	369	3 AAB24051	Aab24051 Human PRO
34	1413	66.3	366	9 AEA39229	Aea39229 GRAL-rela
35	1386	65.0	315	2 AAW37462	Aaw37462 Human Ret
36	1386	65.0	315	8 ADJ58711	Adj58711 Human Ret
37	1386	65.0	315	9 ADY53847	Ady53847 Partial h
38	1386	65.0	315	9 ADZ00211	Adz00211 Human Ret
39	722	33.9	172	2 AAW65118	Aaw65118 Human GDN
40	654	30.7	498	2 AAW84183	Aaw84183 Consensus
41	640.5	30.1	489	2 AAW84298	Aaw84298 Consensus
42	577.5	27.1	460	2 AAW84181	Aaw84181 A GDNFR-a
43	577.5	27.1	464	2 AAW71602	Aaw71602 Rat neut
44	577.5	27.1	464	2 AAW92299	Aaw92299 Rat GDNFR
45	577.5	27.1	464	3 AAY80122	Aay80122 Rat neut

ALIGNMENTS

RESULT 1
AAW37461
ID AAW37461 standard; protein; 397 AA.
XX AAW37461;
XX AC
XX DT 21-MAY-1998 (first entry)
XX DE Mouse Ret ligand RetL3.
XX KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
KW motor neurone disease; multiple sclerosis; infection; meningitis;
KW myelopathy; Croutfeldt-Jakob disease; cranial nerve injury;
KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
KW muscular dystrophy; myasthenia gravis; tumour; therapy.
XX OS Mus musculus.
XX PN WO9744356-A2.
XX PD 27-NOV-1997.
XX PF 07-MAY-1997; 97WO-US007726.
XX PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 11-APR-1997; 97US-0043533P.
(BIOJ) BIOGEN INC.
PI Sanicola-Nadel M, Hession C, Cate RL;
XX WPI; 1998-018431/02.
DR N-PSDB; AAV00249.
XX PT New nucleic acid encoding ret receptor ligands and related proteins -
PT vectors, transformed cells and antibodies, used for promoting cell growth
PT and improving survival of injured cells, especially renal or nerve cells.
PS Claim 2; Page 77-78; 113pp; English.
XX CC This amino acid sequence comprises mouse Ret ligand (RetL), deduced
CC from cDNA clones (see AAV00249) isolated from an EST database and by
CC 5'RACE. Rat and human RetL1, human RetL2 and RetL3 sequences (see

CC AAW37457-60 and AAW37462-63) are also claimed. RetL is a key component of
 CC the Ret signalling pathway that specifically interacts with Ret receptor
 CC protein, triggering Ret dimerisation and/or autophosphorylation of the
 CC Ret tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic
 CC or eukaryotic host cells transfected or transfected with these vectors
 CC are claimed, as well as a method for production of RetL3, its soluble
 CC variants and fusion proteins with a toxin, imageable compound or
 CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
 CC used to promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in renal
 CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
 CC viral or prion infections (e.g. meningitis, myelopathy associated with
 CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
 CC developmental disorders such as Down's syndrome and cerebral palsy, or
 CC conditions involving the peripheral nervous system (Lyme disease,
 CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
 CC deliver toxins etc. to Ret-expressing cells, especially tumours
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 2; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYOH 60
 DB 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYOH 60
 QY 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPA 120
 QY 121 RSLGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCLKFAMLCTLHDKCDRLRKAYG 180
 DB 121 RSLGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCLKFAMLCTLHDKCDRLRKAYG 180
 QY 181 EACSGIRQCRLCLAQRSFPEKAAESHAQGLLPCPCAPEDAGCGRRNTTAPSALPS 240
 DB 181 EACSGIRQCRLCLAQRSFPEKAAESHAQGLLPCPCAPEDAGCGRRNTTAPSALPS 240
 QY 241 VTPNCLDLRFRCADPLCRSLMDFOFTHCPMDILGTGTEQSRCLRAYLGLGTAMTPN 300
 DB 241 VTPNCLDLRFRCADPLCRSLMDFOFTHCPMDILGTGTEQSRCLRAYLGLGTAMTPN 300
 QY 301 FISKVNTVALSCTCRSGNMQDECEQLRSFSONPCLVEIAIAKORFHRQLFSQDADS 360
 DB 301 FISKVNTVALSCTCRSGNMQDECEQLRSFSONPCLVEIAIAKORFHRQLFSQDADS 360
 QY 361 TFSVVOQNSNPALRQPRILPILSFTLPLILLQTLW 397
 DB 361 TFSVVOQNSNPALRQPRILPILSFTLPLILLQTLW 397

RESULT 2
 AAY84591
 ID AAY84591 standard; protein; 397 AA.
 XX
 AC AAY84591;
 XX
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of a human growth factor receptor-alpha precursor.

XX Human; artemin; growth factor; neurotrophic factor; trophic support;
 KW neuron; trigeminal ganglion neuron; nodose ganglion neuron;
 KW superior cervical ganglion neuron; midbrain neuron; Alzheimer's disease;
 KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
 KW Parkinson's disease; Huntington's disease; acute brain injury;
 KW acute spinal cord injury; nervous system tumour; blastoma;
 KW multiple sclerosis; infection; enteric disease; idiopathic constipation;
 KW Parkinson's disease; small cell lung carcinoma.
 XX

OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..28 /note= "signal peptide"
 FT Protein 29..369 /note= "mature protein"
 FT Modified-site 92
 FT /note= "putative N-linked glycosylation site"
 FT Modified-site 145
 FT /note= "putative N-linked glycosylation site"
 FT Modified-site 306
 FT /note= "putative N-linked glycosylation site"
 XX WO200018799-A1.
 XX 06-APR-2000.
 XX 29-SEP-1999; 99WO-US022604.
 XX 29-SEP-1998; 98US-00163283.
 XX 12-NOV-1998; 98US-0108148P.
 XX 22-DEC-1998; 98US-00218698.
 XX (UNIW) UNIV WASHINGTON.
 XX PA
 XX Milbrandt JD, Baloh RH;
 XX WPI; 2000-293109/25.
 XX Isolated artemin growth factor proteins and the nucleic acids that encode
 PT them, useful for treating a range of degenerative neuronal disorders such
 PT as Parkinson's disease and Huntington's disease.
 XX Disclosure; Fig 12; 96pp; English.
 XX The present sequence represents a murine growth factor receptor-alpha
 CC precursor. The specification describes an artemin growth factor protein.
 CC Artemin is a neurotrophic factor that belongs to the GDNF (glial cell
 CC line-derived neurotrophic factor)/neurturin/persephin family of growth
 CC factors and promotes differentiation, maintains mature phenotype and
 CC provides trophic support, promoting growth and survival of neurons.
 CC Artemin promotes the survival of trigeminal ganglion neurons and tyrosine-
 CC hydroxylase-expressing dopaminergic ventral midbrain neurons. Artemin is
 CC the only member of the GDNF family that binds to GFR-alpha (growth factor
 CC receptor-alpha) and activates the GFR-alpha3/RET (Ret protein-tyrosine
 CC kinase) receptor complex and additionally, like GDNF and neurturin,
 CC artemin also binds to and activates GFRalpha1/RET. Artemin polypeptides
 CC and polynucleotides are administered to treat peripheral neuropathy,
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
 CC Huntington's disease, ischemic stroke, acute brain injury, acute spinal
 CC cord injury, a nervous system tumour (e.g. blastoma), multiple
 CC sclerosis, infection or enteric disease (e.g. idiopathic constipation or
 CC constipation associated with Parkinson's disease, spinal cord injury or
 CC use of opiate pain killers). They may also be used to treat a patient
 CC suffering from small cell lung carcinoma
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYOH 60
 DB 1 MGLSWSPRPPLMLLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYOH 60
 QY 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPA 120
 QY 121 RSLGDYELDVSPYEDVTTSKPKWKNLSKLNMLKPDSDCLCLKFAMLCTLHDKCDRLRKAYG 180

Db 121 RSLGDELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLKFAMLCTLHDKCDRLKAYG 180
 QY 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 Db 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTGTCQSRCLRAYLGLIGTAMTPN 300
 Db 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTGTCQSRCLRAYLGLIGTAMTPN 300
 QY 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 Db 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRLOPRLPILSILPILLLQTLW 397
 Db 361 TFSVVOQNSNPALRLOPRLPILSILPILLLQTLW 397

RESULT 3
 AAY15174
 ID AAY15174 standard; protein; 397 AA.
 AC AAY15174;
 XX 07-FEB-2000 (first entry)
 DT Murine GFRalpha3.
 DE Murine GFRalpha3;
 XX Glial-cell-line-derived neurotrophic factor family receptor alpha-3;
 KW probe; homologous DNA; neuronal cell activation; GFRalpha3 ligand;
 KW cell proliferation; cell differentiation; GFRalpha3-containing cell;
 KW Ret-containing cell; peripheral nervous system disease; diabetes;
 KW human immunodeficiency virus; chemotherapeutic agent treatment;
 KW autonomic nervous system dysfunction; transgenic animal.
 XX Mus musculus.
 FH Key
 FT Peptide
 FT 1..27 Location/Qualifiers
 FT /label= signal_peptide
 FT Modified-site 92..95
 FT /note= "Potential glycosylation site"
 FT Modified-site 145..148
 FT /note= "Potential glycosylation site"
 FT Region 392..397
 FT /note= "C-terminal hydrophobic sequence associated with GPI-anchoring"
 FT WO9949039-A2.
 XX 30-SEP-1999.
 XX 19-MAR-1999; 99WO-US006098.
 XX 23-MAR-1998; 98US-0079124P.
 PR 13-APR-1998; 98US-0081569P.
 XX (GETH) GENENTECH INC.
 XX De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
 XX WPI; 2000-038358/03.
 DR N-PSDB; AAZ29100.
 XX New isolated GFR-alpha3 nucleic acid, used to develop products for
 PT treating diseases or conditions involving peripheral nervous system or
 PT autonomic nervous system.
 XX Example 1; Fig 1; 112pp; English.
 XX

The present sequence is the full length mouse glial-cell-line-derived
 CC neurotrophic factor family receptor alpha-3 (GFRalpha3). This has
 CC sequence identity with GFRalpha1. GFRalpha3 DNA or its fragments can be
 CC used as a probe to screen for homologous DNA. GFRalpha3 possesses neuronal
 CC cell activation property. GFRalpha3 ligands can be used to stimulate
 CC proliferation, growth, survival, differentiation, metabolism or
 CC regeneration of GFRalpha3- and Ret-containing cells. They can be useful
 CC in the treatment of peripheral nervous system diseases, eg. those
 CC associated with diabetes, human immunodeficiency virus, or
 CC chemotherapeutic agent treatments. Agonist or antagonists of GFRalpha3
 CC can be used to treat autonomic nervous system dysfunctions. The products
 CC can also be used for detection, diagnosis and production of transgenic
 CC animals
 XX Sequence 397 AA;
 SQ
 Query Match 100.0%; Score 2131; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSNSPRPPLMLLLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYQH 60
 Db 1 MGLSNSPRPPLMLLLVLSLMLPLGAGNSLATENFVNSCTQARKKCEANPACKAAYQH 60
 QY 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPA 120
 Db 61 LGSCTSSLSRPLPLEESAMSDCLEAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPA 120
 QY 121 RSLGDELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLKFAMLCTLHDKCDRLKAYG 180
 Db 121 RSLGDELDVSPYEDVTTSKPKWNLKLNMLKPDSDCLKFAMLCTLHDKCDRLKAYG 180
 QY 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 Db 181 EACSGIRCORHLCLAQLRSEFFKAAESHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTGTCQSRCLRAYLGLIGTAMTPN 300
 Db 241 VTPNCLDLRSFCRADPLCRSLMDFOFTHCHPMDILGTGTCQSRCLRAYLGLIGTAMTPN 300
 QY 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 Db 301 FISKVNTTVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRLOPRLPILSILPILLLQTLW 397
 Db 361 TFSVVOQNSNPALRLOPRLPILSILPILLLQTLW 397
 RESULT 4
 ADJ58709
 ID ADJ58709 standard; protein; 397 AA.
 XX ADJ58709;
 XX 06-MAY-2004 (first entry)
 DT Murine retL3 protein.
 DE Tissue growth; retL protein; organ failure; foetal malformation;
 KW tumour growth; renal tissue; cytostatic; vulnerary; nephrotropic; murine.
 XX Mus sp.
 XX US6677135-B1.
 PN 13-JAN-2004.
 PD 06-NOV-1998; 98US-00187906.
 XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.

PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 XX WPI; 2004-079845/08.
 DR N-PSDB; ADJ58708.
 XX
 XX New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
 PT treating diseases or conditions associated with aberrant expression or
 PT activity of the Ret ligand, such as organ failure, fetal malformations
 PT and tumor growth.
 XX
 XX Claim 1; SEQ ID NO 17; 66pp; English.
 XX
 CC The present invention relates to nucleotide and amino acid sequences
 CC which promote tissue growth and methods for modulating tissue growth. The
 CC invention also relates to retL proteins and polynucleotides encoding such
 CC proteins. RetL proteins interact with a receptor protein Ret to trigger
 CC dimerisation and/or autophosphorylation of the tyrosine kinase domain of
 CC the receptor protein Ret. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of diseases or
 CC conditions associated with aberrant expression or activity of the Ret
 CC ligand, such as organ failure, foetal malformations and tumour growth and
 CC for promoting regeneration or survival of damaged renal tissue. The
 CC present sequence is murine retL3 protein of the invention.
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 8; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 DB 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 QY 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYTVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYTVHPA 120
 QY 121 RSLGDIYELDVSPYEDVTTSKPKWQNLKLNMLKPDSDILCKFAMLCITLHDKCDRLKAYG 180
 DB 121 RSLGDIYELDVSPYEDVTTSKPKWQNLKLNMLKPDSDILCKFAMLCITLHDKCDRLKAYG 180
 QY 181 EACSGIRCQRHLCIAQLRSFFFEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGIRCQRHLCIAQLRSFFFEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSCLRAYLGLIGTAMTNP 300
 DB 241 VTPNCLDLRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSCLRAYLGLIGTAMTNP 300
 QY 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKRFRHQLFSQDWADS 360
 DB 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKRFRHQLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRQLPRLPILSILPLLILQTLW 397
 DB 361 TFSVVOQNSNPALRQLPRLPILSILPLLILQTLW 397

RESULT 5

ADY53845

ID ADY53845 standard; protein; 397 AA.

XX ADY53845;

XX ADY53845;

DT 05-MAY-2005 (first entry)

XX

DE Mouse retL3 protein.
 XX
 KW DNA purification; immune stimulation; ret ligand.
 XX
 OS Mus sp.
 XX
 PN US6861509-B1.
 XX
 PD 01-MAR-2005.
 XX
 PF 21-JAN-2000; 2000US-00489407.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 XX (BIOJ) BIOGEN INC.
 PA
 XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 PI
 XX WPI; 2005-201184/21.
 DR N-PSDB; ADY53844.
 XX
 DR New anti-Ret ligand (RetL) antibody, useful for treating acute renal
 XX failure, acute nephritis, chronic renal failure, nephritic syndrome, as
 PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.
 PT
 XX Disclosure; SEQ ID NO 17; 66pp; English.
 PS
 XX The invention relates to an antibody produced by a hybridoma selected
 CC from the group consisting of AA.FP9 and AA.GE7.3. The antibody is used to
 CC stimulate neural and renal cell growth. This sequence corresponds to a
 CC protein sequence of the invention.
 XX
 SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 9; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 DB 1 MGLSWSPRPPLMILLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYOH 60
 QY 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYTVHPA 120
 DB 61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRMKHQATCLDIYTVHPA 120
 QY 121 RSLGDIYELDVSPYEDVTTSKPKWQNLKLNMLKPDSDILCKFAMLCITLHDKCDRLKAYG 180
 DB 121 RSLGDIYELDVSPYEDVTTSKPKWQNLKLNMLKPDSDILCKFAMLCITLHDKCDRLKAYG 180
 QY 181 EACSGIRCQRHLCIAQLRSFFFEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGIRCQRHLCIAQLRSFFFEKAESAHAQGLLLCPAPEDAGCGERRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSCLRAYLGLIGTAMTNP 300
 DB 241 VTPNCLDLRSFCRADPLCRSLRMDFTQTHCPMDILGTCAEQSCLRAYLGLIGTAMTNP 300
 QY 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKRFRHQLFSQDWADS 360
 DB 301 FISKVNTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKRFRHQLFSQDWADS 360
 QY 361 TFSVVOQNSNPALRQLPRLPILSILPLLILQTLW 397
 DB 361 TFSVVOQNSNPALRQLPRLPILSILPLLILQTLW 397

RESULT 6

ADZ00209
 ID ADZ00209 standard; protein; 397 AA.
 XX
 AC ADZ00209;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Mouse Ret ligand 3 (RetL3), SEQ ID NO:17.
 XX
 KW Cell growth; development; signal transduction; neurological disease;
 KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
 KW cancer; neoplasm; cytostatic; RetL3;
 KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
 KW GDNF family receptor alpha 3; GFRA3.
 XX
 OS Mus sp.
 XX
 PN US2005080235-A1.
 XX
 PD 14-APR-2005.
 XX
 PP 23-SEP-2003; 2003US-00668936.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US0007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 PA (SANI/) SANICOLA-NADEL M.
 PA (HESS/) HESSION C.
 PA (CATE/) CATE R L.
 PA (WORL/) WORLEY D S.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 XX
 DR WPI; 2005-305025/31.
 DR N-PSDB; ADZ00208.
 XX
 FT New polypeptide sequence that interacts with a receptor protein Ret to
 PT trigger dimerization or autophosphorylation, useful in preparing a
 PT composition for treating neurodegenerative disorders, e.g., Alzheimer's
 PT disease.
 XX
 PS Claim 1; SEQ ID NO 17; 67pp; English.
 XX
 CC The invention relates to the murine and human RetL3 (Ret ligand 3)
 CC proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least
 CC 80% identical to murine or human RetL3. The invention also discloses
 CC other RetL proteins such as rat RetL1, human RetL1, human RetL2,
 CC fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
 CC encoding these RetL proteins or protein fragments. Like other RetL
 CC proteins, the RetL3 proteins of the invention interact with the Ret
 CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
 CC triggering Ret receptor dimerization or autophosphorylation. The Ret
 CC receptor is expressed during development in a variety of tissues,
 CC including the peripheral and central nervous systems and the kidney. It
 CC is also expressed in some cancers. RetL proteins such as the murine and
 CC human RetL3 proteins, and RetL polynucleotides may be used for
 CC stimulating Ret receptor signaling, thereby promoting renal or neuronal
 CC cell growth or survival and minimizing damage to such tissues after
 CC various insults. They may therefore be used to treat renal disorders
 CC (e.g., renal failure, renal tube defects and renal trauma) or
 CC neurological disorders including neurodegenerative disorders (e.g.,
 CC Alzheimer's disease), bacterial or viral diseases of the nervous system
 CC (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
 CC or trauma) and developmental neural disorders (e.g., mental retardation).
 CC Conversely, antibodies against RetL may be used to block RetL-Ret
 CC receptor signal transduction for inhibiting tumor growth, fusion proteins
 CC comprising a RetL protein are useful for targeting a drug to Ret receptor

CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
 CC also be used in medical imaging. The present sequence represents a
 CC specifically claimed full-length murine RetL3 protein encoded by cDNA
 CC isolated in the invention.
 XX
 SQ Sequence 397 AA;
 Query Match 100.0%; Score 2131; DB 9; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.5e-198;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSWSPRPPLMLILLVLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAQYH 60
 DB 1 MGLSWSPRPPLMLILLVLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAQYH 60
 QY 61 LGSCTSSLRPLPLEESAMSDCLEAEQLRNSLIDCRHRRMKHOATCLDIYVTVHPA 120
 DB 61 LGSCTSSLRPLPLEESAMSDCLEAEQLRNSLIDCRHRRMKHOATCLDIYVTVHPA 120
 QY 121 RSLGDYELDVSPYEDVTTSKPMKNLSKLNMLKPDSDLCIKFAMLCITLHDKCDRLRKAYG 180
 DB 121 RSLGDYELDVSPYEDVTTSKPMKNLSKLNMLKPDSDLCIKFAMLCITLHDKCDRLRKAYG 180
 QY 181 EACSGIRCQRHLCIAQLRSFFFEKAAESHAQGLLLCPACAPEDACGRRRNTIAPSCALPS 240
 DB 181 EACSGIRCQRHLCIAQLRSFFFEKAAESHAQGLLLCPACAPEDACGRRRNTIAPSCALPS 240
 QY 241 VTPNCUDLRSFCRADPLCRSLRMDFTQCHPMIDILGTCATEQSRCLRAYILGLIGTAMTPN 300
 DB 241 VTPNCUDLRSFCRADPLCRSLRMDFTQCHPMIDILGTCATEQSRCLRAYILGLIGTAMTPN 300
 QY 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQDWADS 360
 DB 301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQDWADS 360
 QY 361 TFSVVOQNSNPALRLQPLRPILPILPILPILPILPILPILPILPILPILPILPILPIL 397
 DB 361 TFSVVOQNSNPALRLQPLRPILPILPILPILPILPILPILPILPILPILPILPILPIL 397
 RESULT 7
 AAW84182
 ID AAW84182 standard; protein; 397 AA.
 XX
 AC AAW84182;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE A GDNFR-alpha-related protein 3 (GRR3).
 XX
 KW Rat; glial cell-line derived neurotrophic factor receptor; GDNFR;
 KW glial cell line-derived neurotrophic factor; GDNF; neurturin;
 KW signal transduction; dopaminergic nerve cell; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
 KW gene therapy; GDNFR-related protein 3; GRR3.
 XX
 OS Rattus sp.
 XX
 PN WO9854213-A2.
 XX
 PD 03-DEC-1998.
 XX
 PP 27-APR-1998; 98WO-US008486.
 XX
 PR 30-MAY-1997; 97US-00866354.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Fox GM, Jing S, Wen D;
 XX
 DR WPI; 1999-080806/07.

DR N-PSDB; AAV99331.
 XX New isolated glial cell line-derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. improperly functioning dopaminergic
 FT nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
 PT lateral sclerosis.
 XX
 XX Claim 51; Fig 17; 318pp; English.
 XX
 CC The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3). The
 CC protein has similar functions to GDNFR. GDNFR proteins are functionally
 CC characterised by the ability to bind glial cell line-derived neurotrophic
 CC factor (GDNF) and/or neurturin specifically, and to act as part of a
 CC molecular complex which mediates or enhances the signal transduction
 CC affects of GDNF and/or neurturin. The proteins can be used for treating
 CC Alzheimer's disease or amyotrophic lateral sclerosis. They can also be
 CC used for treating neurological disorders associated with diabetes,
 CC glaucoma or other diseases and conditions involving retinal ganglion cell
 CC degeneration, sensory neuropathy caused by injury to, insults to, or
 CC degeneration of, sensory neurons, pathological conditions, or disease or
 CC injury-related retinopathies. The products can also be used for
 CC detection, diagnosis, drug screening and gene therapy
 XX
 XX Sequence 397 AA;
 SQ
 Query Match 92.5%; Score 1972; DB 2; Length 397;
 Best Local Similarity 92.9%; Pred. No. 1e-182;
 Matches 369; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
 QY 1 MGLSWPRPLMILLVLSMLPLGAGNSLATENRFVNSCTQARKKCEANPACAAAYOH 60
 DB 1 MGLSRSPRPPLVILLVLSMLPLGTGNSLPTENLNVNSCTQARKKCEANPACAAAYOH 60
 QY 61 LGSCTSSLRPLPEBSAMSADCLEAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPA 120
 DB 61 LDSCTPSLSPLPSGESATSAACLEAAQQLRNSLLIDCRHRMKHQATCLDIYTVHPV 120
 QY 121 RSLGVDYELVSPYEDVTTSKPMKQNLKMLKPDSDCLKFMALCTLDKCDRLKAYG 180
 DB 121 RSLGVDYELVSPYEDVTTSKPMKQNLKMLKPDSDCLKFMALCTLDKCDRLKAYG 180
 QY 181 EACSGIRCORHLCLAOIRSFPEKAESHAQGLLLCPAPEDAGCGRRNTIAPSCALPS 240
 DB 181 EACSGIRCORHLCLAOIRSFPEKAESHAQGLLLCPAPEDAGCGRRNTIAPSCALPS 240
 QY 241 VTPNCLDLRSFCRADPLCRSLMDFTQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTN 300
 DB 241 VAPNCLDLRSFCRADPLCRSLMDFTQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTN 300
 QY 301 FISKVNTVALSTCRSGNLODECEQLERSFQNPCLVEATAAKMRFHQRLFQSDWADS 360
 DB 301 FISKVNTVALSTCRSGNLODECEQLERSFQNPCLVEATAAKMRFHQRLFQSDWADS 360
 QY 361 TFSVVOQNSPALRLQPRLPILSILPILLQTLW 397
 DB 361 TFSVVOQNSPALRLQPRLPILSILPILLQTLW 397
 RESULT 8
 AAY15182
 XX AAY15182 standard; protein; 888 AA.
 ID
 XX AAY15182;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE GD-GFRalpha3-Rse-gd chimeric receptor.
 XX
 KW GD-GFRalpha3-Rse-gd chimeric receptor; gd epitope tag; murine GFRalpha3;
 KW GPI signal; human GFRalpha3; Rse tyrosine kinase receptor; pSV1 vector;
 KW recombinant PCR; SV40 promoter; agonist antibody; natural ligand.

XX Synthetic.
 OS
 XX Location/Qualifiers
 FH Key 110..386
 FT Region /note= "Ligand binding region"
 FT
 XX
 XX WO9949039-A2.
 XX
 XX 30-SEP-1999.
 PD
 XX 19-MAR-1999; 99WO-US006098.
 PF
 XX 23-MAR-1998; 98US-0079124P.
 PR
 XX 13-APR-1998; 98US-0081569P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
 PI WPI; 2000-038358/03.
 XX
 DR New isolated GFR-alpha3 nucleic acid, used to develop products for
 XX treating diseases or conditions involving peripheral nervous system or
 PT autonomic nervous system.
 PT
 XX
 XX Claim 9; Page 107-110; 112pp; English.
 PS
 XX The present sequence is GD-GFRalpha3-Rse-gd chimeric receptor. This was
 CC constructed with the gd epitope tag followed by the murine GFRalpha3
 CC extracellular domain (less the GPI signal; preferably the human
 CC GFRalpha3) followed by the transmembrane and intracellular domain of the
 CC Rse tyrosine kinase receptor and another gd epitope tag. This construct
 CC was assembled by recombinant PCR into a pSV1 vector under the control of
 CC the SV40 promoter. This is used in an assay to identify agonist
 CC antibodies and a natural ligand for mammalian GFRalpha3
 XX
 XX Sequence 888 AA;
 SQ
 Query Match 88.2%; Score 1880; DB 3; Length 888;
 Best Local Similarity 94.1%; Pred. No. 2.8e-173;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;
 QY 25 LGAGNSLATENRFVNSCTQARKKCEANPACAAAYOHLSGCTSSLSRPLPEBSAMSADCL 84
 DB 54 LEAGNSLATENRFVNSCTQARKKCEANPACAAAYOHLSGCTSSLSRPLPEBSAMSADCL 113
 QY 85 EAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPARSLGVDYELVSPYEDVTTSKPMK 144
 DB 114 EAAEQLRNSSLIDCRHRMKHQATCLDIYTVHPARSLGVDYELVSPYEDVTTSKPMK 173
 QY 145 NLSKLNMLKPDSDCLKFMALCTLDKCDRLKAYGACSGIRCORHLCLAOIRSFPEKA 204
 DB 174 NLSKLNMLKPDSDCLKFMALCTLDKCDRLKAYGACSGIRCORHLCLAOIRSFPEKA 233
 QY 205 AESHAQGLLLCPAPEDAGCGRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSLMD 264
 DB 234 AESHAQGLLLCPAPEDAGCGRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSLMD 293
 QY 265 FQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTNFISKVNTVALSTCRSGNLODE 324
 DB 294 FQTHCHPMDILGTCAEQSRCLRAYLIGLTAMTNFISKVNTVALSTCRSGNLODE 353
 QY 325 CEQLERSFQNPCLVEATAAKMRFHQRLFQSDWADSTFSVVOQNSPALRL-----LQP 378
 DB 354 CEQLERSFQNPCLVEATAAKMRFHQRLFQSDWADSTFSVVOQNSPALRAWVPVLGV 413
 QY 379 RLPILSILPILLQ 394
 DB 414 LVALVTAAALAILLR 429
 RESULT 9

AAW37465
ID AAW37465 standard; protein; 346 AA.
AC AAW37465;
XX
XX
XX 21-MAY-1998 (first entry)
XX
XX Mouse Ret ligand retL3 partial sequence.
XX
XX Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
XX cell growth; renal cell; nerve cell; renal failure; nephritis;
XX kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
XX motor neurone disease; multiple sclerosis; infection; meningitis;
XX myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
XX spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
XX muscular dystrophy; myasthenia gravis; tumour; therapy.
XX
XX Mus musculus.
XX
XX WO9744356-A2.
XX
XX 27-NOV-1997.
XX
XX 07-MAY-1997; 97WO-US007726.
XX
XX 08-MAY-1996; 96US-0017427P.
XX 07-JUN-1996; 96US-0019300P.
XX 16-JUL-1996; 96US-0021859P.
XX 11-APR-1997; 97US-0043533P.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Sanicola-Nadel M, Hession C, Cate RL;
XX
XX WPI; 1998-018431/02.
XX N-PSDB; AAV00256.
XX
XX New nucleic acid encoding ret receptor ligands and related proteins -
XX vectors, transformed cells and antibodies, used for promoting cell growth
XX and improving survival of injured cells, especially renal or nerve cells.
XX
XX Disclosure; Page 73-74; 113pp; English.
XX
XX This polypeptide comprises a partial sequence of mouse Ret ligand RetL3,
XX deduced from EST AA050083 cDNA (see AAV00256). A full-length mouse RetL3
XX sequence (see AAW37461) was also obtained. Rat, mouse and human RetL1,
XX RetL2 and RetL3 cDNA sequences (see AAV00245-51) and encoded polypeptides
XX (see AAW37457-63) are claimed and can be used in methods for promoting
XX cell growth and improving survival of cells, especially renal or neural
XX cells
XX
XX Sequence 346 AA;
XX
XX Query Match 83.2%; Score 1774; DB 2; Length 346;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-163;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 68 LSRPLPESAMSDCLAEAEQLRNSLIDCRHRMKHQATCLDIYTWVHPARSIGDYE 127
XX 17 LSRPLPESAMSDCLAEAEQLRNSLIDCRHRMKHQATCLDIYTWVHPARSIGDYE 76
XX 128 LDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCLKFMALCTLHDKCDRLKAYGEACSGIR 187
XX 77 LDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCLKFMALCTLHDKCDRLKAYGEACSGIR 136
XX 188 CQRHLCLAIRSPFEKAESAAGLLCPCAPEDAGGERRNTIAPSCALPVTNCLD 247
XX 137 CQRHLCLAIRSPFEKAESAAGLLCPCAPEDAGGERRNTIAPSCALPVTNCLD 196
XX 248 LRSFCRADPLCRSLRMDFTQCHPMDILGTGTCATEQSRCLRAYLGLGTATWPNFISKVNT 307
XX 197 LRSFCRADPLCRSLRMDFTQCHPMDILGTGTCATEQSRCLRAYLGLGTATWPNFISKVNT 256

QY 308 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHQLFSQDWDSTFVSQQ 367
XX
Db 257 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHQLFSQDWDSTFVSQQ 316
XX
QY 368 QNSNPALRQPLRPILSFSILPLILLOTLM 397
XX
Db 317 QNSNPALRQPLRPILSFSILPLILLOTLM 346
XX
RESULT 10
ADJ58707
ID ADJ58707 standard; protein; 346 AA.
XX
XX ADJ58707;
AC
XX 06-MAY-2004 (first entry)
DT
XX Murine retL3 partial protein.
DE
XX
XX Tissue growth; retL protein; organ failure; foetal malformation;
XX tumour growth; renal tissue; cytostatic; vulnerary; nephrotropic; murine.
KW
XX Mus sp.
OS
XX US6677135-B1.
XX
XX 13-JAN-2004.
XX
XX 06-NOV-1998; 98US-00187906.
XX
XX 08-MAY-1996; 96US-0017427P.
XX 07-JUN-1996; 96US-0019300P.
XX 16-JUL-1996; 96US-0021859P.
XX 23-AUG-1996; 96US-0023444P.
XX 11-APR-1997; 97US-0043533P.
XX 07-MAY-1997; 97WO-US007726.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
XX WPI; 2004-079845/08.
XX N-PSDB; ADJ58706.
XX
XX New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
XX treating diseases or conditions associated with aberrant expression or
XX activity of the Ret ligand, such as organ failure, fetal malformations
XX and tumor growth.
XX
XX Disclosure; SEQ ID NO 15; 66pp; English.
XX
XX The present invention relates to nucleotide and amino acid sequences
XX which promote tissue growth and methods for modulating tissue growth. The
XX invention also relates to retL proteins and polynucleotides encoding such
XX proteins. RetL proteins interact with a receptor protein Ret to trigger
XX dimerisation and/or autophosphorylation of the tyrosine kinase domain of
XX the receptor protein Ret. The methods and compositions of the present
XX invention are useful for the diagnosis and/or treatment of diseases or
XX conditions associated with aberrant expression or activity of the Ret
XX ligand, such as organ failure, foetal malformations and tumour growth and
XX for promoting regeneration or survival of damaged renal tissue. The
XX present sequence is murine retL3 partial protein of the invention.
XX
XX Sequence 346 AA;
XX
XX Query Match 83.2%; Score 1774; DB 8; Length 346;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-163;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 68 LSRPLPESAMSDCLAEAEQLRNSLIDCRHRMKHQATCLDIYTWVHPARSIGDYE 127
XX 17 LSRPLPESAMSDCLAEAEQLRNSLIDCRHRMKHQATCLDIYTWVHPARSIGDYE 76

QY 128 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCCTLDKCDRLKAYGEACSGIR 187
 DB 77 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCCTLDKCDRLKAYGEACSGIR 136
 QY 188 CORHLCLAQRLSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 247
 DB 137 CORHLCLAQRLSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 307
 DB 197 LRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 256
 QY 308 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQDWADSTFSVVOQ 367
 DB 257 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQDWADSTFSVVOQ 316
 QY 368 QNSNPALRLQPLRPLILSFSILPLILLQTLW 397
 DB 317 QNSNPALRLQPLRPLILSFSILPLILLQTLW 346
 RESULT 11
 ID ADY53843 standard; protein; 346 AA.
 XX ADY53843;
 AC
 XX 05-MAY-2005 (first entry)
 DT
 DE Partial mouse retL3 protein.
 XX
 XX DNA purification; immune stimulation; ret ligand.
 XX
 XX Mus sp.
 OS
 PN US6861509-B1.
 XX
 XX 01-MAR-2005.
 PD
 XX
 PF 21-JAN-2000; 2000US-00489407.
 XX
 XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 XX (BIOJ) BIOGEN INC.
 XX
 XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 PI
 XX WPI; 2005-201184/21.
 DR N-PSDB; ADY53842.
 XX
 XX New anti-Ret ligand (RetL) antibody, useful for treating acute renal
 PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as
 PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.
 XX
 XX Disclosure; SEQ ID NO 15; 66pp; English.
 PS
 XX The invention relates to an antibody produced by a hybridoma selected
 CC from the group consisting of AA.FF9 and AA.GE7.3. The antibody is used to
 CC stimulate neural and renal cell growth. This sequence corresponds to a
 CC protein sequence of the invention.
 XX
 XX Sequence 346 AA;
 SQ
 Query Match 83.2%; Score 1774; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 LSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYVTVHPARSLGDYE 127
 DB 17 LSRPLPLEESAMSDCLEAAEQRLNSSLIDCRCHRRMKHQATCLDIYVTVHPARSLGDYE 76
 QY 128 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCCTLDKCDRLKAYGEACSGIR 187
 DB 77 LDVSPYEDVTTSKPKWKNLSKLNMLKPDSDLCCLKFAMLCCTLDKCDRLKAYGEACSGIR 136
 QY 188 CORHLCLAQRLSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 247
 DB 137 CORHLCLAQRLSPFFKAEASHAQLLPCAPEDAGCGERRNTIAPSCALPSVTPNCLD 196
 QY 248 LRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 307
 DB 197 LRSFCRADPLCRSLRMDFTQCHPMDILGTCAEQSRCLRAYLGLIGTAMTNPFSKVT 256
 QY 308 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQDWADSTFSVVOQ 367
 DB 257 TVALSCTCRSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRLQFSQDWADSTFSVVOQ 316
 QY 368 QNSNPALRLQPLRPLILSFSILPLILLQTLW 397
 DB 317 QNSNPALRLQPLRPLILSFSILPLILLQTLW 346
 RESULT 12
 ID ADZ00207 standard; protein; 346 AA.
 XX ADZ00207;
 AC
 XX 30-JUN-2005 (first entry)
 DT
 DE Mouse Ret ligand 3 (RetL3) fragment, SEQ ID NO:15.
 XX
 XX Cell growth; development; signal transduction; neurological disease;
 KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
 KW cancer; neoplasm; cytostatic; RetL3;
 KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
 KW GDNF family receptor alpha 3; GFR3.
 XX
 XX Mus sp.
 OS
 XX US2005080235-A1.
 PN
 XX 14-APR-2005.
 PD
 XX 23-SEP-2003; 2003US-00668936.
 PF
 XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 23-AUG-1996; 96US-0023444P.
 PR 11-APR-1997; 97US-0043533P.
 PR 07-MAY-1997; 97WO-US007726.
 PR 06-NOV-1998; 98US-00187906.
 XX
 XX (SANI/) SANICOLA-NADEL M.
 PA (HESS/) HESSION C.
 PA (CATE/) CATE R L.
 PA (WORL/) WORLEY D S.
 XX
 XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
 PI
 XX WPI; 2005-305025/31.
 DR N-PSDB; ADZ00206.
 DR
 XX New polypeptide sequence that interacts with a receptor protein Ret to
 PT trigger dimerization or autophosphorylation, useful in preparing a
 PT composition for treating neurodegenerative disorders, e.g., Alzheimer's
 PT disease.
 XX
 XX Disclosure; SEQ ID NO 15; 67pp; English.
 PS

XX The invention relates to the murine and human RetL3 (Ret ligand 3)
 CC proteins (AD200209 and AD200213, respectively) and to proteins at least
 CC 80% identical to murine or human RetL3. The invention also discloses
 CC other RetL proteins such as rat RetL1, human RetL1, human RetL2,
 CC fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
 CC encoding these RetL proteins or protein fragments. Like other RetL
 CC proteins, the RetL3 proteins of the invention interact with the Ret
 CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
 CC triggering Ret receptor dimerization or autophosphorylation. The Ret
 CC receptor is expressed during development in a variety of tissues,
 CC including the peripheral and central nervous systems and the kidney. It
 CC is also expressed in some cancers. RetL proteins such as the murine and
 CC human RetL3 proteins, and RetL polynucleotides may be used for
 CC stimulating Ret receptor signaling, thereby promoting renal or neuronal
 CC cell growth or survival and minimizing damage to such tissues after
 CC various insults. They may therefore be used to treat renal disorders
 CC (e.g., renal failure, renal tube defects and renal trauma) or
 CC neurological disorders including neurodegenerative disorders (e.g.,
 CC Alzheimer's disease), bacterial or viral diseases of the nervous system
 CC (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
 CC or trauma) and developmental neural disorders (e.g., mental retardation).
 CC Conversely, antibodies against RetL may be used to block RetL-Ret
 CC receptor signal transduction for inhibiting tumor growth, fusion proteins
 CC comprising a RetL protein are useful for targeting a drug to Ret receptor
 CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
 CC also be used in medical imaging. The present sequence represents a murine
 CC RetL3 fragment encoded by a murine RetL3 partial cDNA initially
 CC identified by a search of an expressed sequence tag (EST) database using
 CC a rat RetL peptide sequence, and isolated from the EST clones AA049894
 CC and AA050083.

XX Sequence 346 AA;

Query Match 83.2%; Score 1774; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.6e-163;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 LSRPLPEESAMGADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 127
 Db 17 LSRPLPEESAMGADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGDYE 76
 QY 128 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
 Db 77 LDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136
 QY 188 CORHLCLAQRLSPFEKAEASHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCID 247
 Db 137 CORHLCLAQRLSPFEKAEASHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNCID 196
 QY 248 LRSGFCRADPLCRSLMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSVNT 307
 Db 197 LRSGFCRADPLCRSLMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSVNT 256
 QY 308 TVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMFRHQLPSQDWDSTFSVQ 367
 Db 257 TVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMFRHQLPSQDWDSTFSVQ 316
 QY 368 QNSNPALRLQPLPILSFLPILLOTLW 397
 Db 317 QNSNPALRLQPLPILSFLPILLOTLW 346

RESULT 13

AAW65116

ID AAW65116 standard; protein; 400 AA.

XX

AAW65116;

XX

DT 28-SEP-1998 (first entry)

XX

DE Human GDNF alpha-3 receptor protein #1.

XX

KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Protein 1..400
 FT /label= GDNF alpha-3
 FT /notes= "Partial sequence"
 XX
 PN EP846764-A2.
 XX
 PD 10-JUN-1998.
 XX
 PF 20-NOV-1997; 97EP-00309375.
 XX
 PR 27-NOV-1996; 96GB-00024677.
 PR 09-MAY-1997; 97GB-00009463.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Lawrence GMP;
 DR WPI; 1998-299980/27.
 DR N-PSDB; AAV35364.
 XX
 PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used
 PT to treat neuro degenerative diseases, muscular diseases and nerve and
 PT muscle trauma and in diagnostic assays.
 XX
 PS Claim 4; Fig 2; 22pp; English.

XX This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat
 CC e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic
 CC lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's
 CC disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases
 CC (including the muscular dystrophies) and nerve and muscle trauma and in
 CC diagnostic assays for such conditions

SQ Sequence 400 AA;

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
 Best Local Similarity 77.8%; Pred. No. 4.9e-151;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
 QY 7 PRPP-LLMTLLVLSLWPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSC 65
 Db 9 PLPPVVLMLLLPLPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAVHLDSC 68
 QY 66 SLSRPLPEESAMGADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGD 125
 Db 69 SSISTPLPEEPPSPADCLAEAEQRLNSLIDCRCHRRMKHQATCLDIYTWVHPARSLGN 128
 QY 126 YELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
 Db 129 YELDVSPYEDTVTSKPKWKNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 188
 QY 186 IRCQRHLCLAQRLSPFEKAEASHAQGLLLCPAPEDAGCGERRNTIAPSCALPSVTPNC 245
 Db 189 PHCQRHVCLRLTLTFEKAEPHAQGLLLCPAPEDAGCGERRNTIAPNCALPPVAPNC 248
 QY 246 LDRSFCRADPLCRSLMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSV 305
 Db 249 LEILRLCFSDPLCRSLMDFOQTHCHPMDILGTCAEQSLRAYLGLIGTAMTNPFIKSV 308
 QY 306 NTTVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMFRHQLPSQDWDSTFSV 365
 Db 309 NTSVALSTCTCRSGNLQDECEQLERSFSQNPCLVRAIAAKMFRHQLPSQDWDSTFSV 368

QY 366 OQNSNPALRQLPRLPILSILPLILQLTLW 397
 Db 369 AHQENPAVRPQWPVPSLFSCTLPILLLSLW 400

RESULT 14
 AAW37463
 ID AAW37463 standard; protein; 400 AA.
 AC AAW37463;
 XX
 XX 21-MAY-1998 (first entry)
 XX
 XX Human Ret ligand RetL3.
 XX
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
 KW motor neurone disease; multiple sclerosis; infection; meningitis;
 KW myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
 KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
 KW muscular dystrophy; myasthenia gravis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO9744356-A2.
 XX
 XX 27-NOV-1997.
 XX
 XX 07-MAY-1997; 97WO-US007726.
 XX
 XX 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 11-APR-1997; 97US-0043533P.
 XX
 XX (BIOJ) BIOGEN INC.
 PA
 XX
 XX Sanicola-Nadel M, Hession C, Cate RL;
 PI
 XX WPI; 1998-018431/02.
 DR N-PSDB; AAV00251.
 DR
 XX
 XX New nucleic acid encoding ret receptor ligands and related proteins -
 PT vectors, transformed cells and antibodies, used for promoting cell growth
 PT and improving survival of injured cells, especially renal or nerve cells.
 XX
 XX Claim 2; Page 85-86; 113pp; English.

CC This amino acid sequence comprises human Ret ligand (RetL) RetL3, deduced
 CC from cDNA clones (see AAV00251) isolated from a adult heart and spinal
 CC cord libraries. Rat and human RetL1, human RetL2 and mouse RetL3
 CC sequences (see AAW37457-62) are also claimed. Human RetL3 is 34.3%
 CC identical to human RetL1, 34.9% identical to human RetL2 and 76.8%
 CC identical to murine RetL3. Ret ligand is a key component of the Ret
 CC signalling pathway that specifically interacts with Ret receptor protein,
 CC triggering Ret dimerisation and/or autophosphorylation of the Ret
 CC tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic or
 CC eukaryotic host cells transformed or transfected with these vectors are
 CC claimed, as well as a method for production of RetL3, its soluble
 CC variants and fusion proteins with a toxin, imageable compound or
 CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
 CC used to promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in renal
 CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
 CC viral or prion infections (e.g. meningitis, myelopathy associated with
 CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
 CC developmental disorders such as Down's syndrome and cerebral palsy, or
 CC conditions involving the peripheral nervous system (Lyme disease,
 CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
 CC deliver toxins etc. to Ret-expressing cells, especially tumours

SQ Sequence 400 AA;
 Query Match 77.3%; Score 1646.5; DB 2; Length 400;
 Best Local Similarity 77.8%; Pred. No. 4.9e-151;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY 7 PRPP-LLMILLVLSMLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSGT 65
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 Db 9 PLPPVVLMLLLLPSPPLAAGDPLPTESRLMNSCLQARRKCCQADPTCSAAYHLDSCST 68
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 66 SSLSRPLPLESAMSADCLEAAEQLRNSSLIDCHRRMKHQATCLDIYWTVHPARSLGD 125
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKQVACLDIYWTVHRRASLGN 128
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 126 YELDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCKPAMLCITLHDKCDRLKAYGEACSG 185
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 129 YELDVSPYEDVTTSKPKWNLSKLNMLKPDSDCLCKPAMLCITLHDKCDRLKAYGEACSG 188
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 186 IRCQRHLCLAOILRSFFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTNFC 245
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 189 PHCQRHVCLRQLLTFEKAAPHAQGLLLCPCAPNDRCGERRRNTIAPNCALPPVAFNFC 248
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 246 LDLRSFCRADPLCRSLMDFTQCHPMIDILGTCAEQSRCLRAYLGLGTAMTNPFIISKV 305
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 249 LELRLCFSDPLCRSLVDFQTHCPMDILGTCAEQSRCLRAYLGLGTAMTNPFIISNV 308
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 306 NTTVALSCTCRSGNLODECEQLRSFSONPCLVEAIAAKMRFHQLFSQDWADSTFVSV 365
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 309 NTSVALSCTCRSGNLODECEMLEGFFSHNPCLTEAIAAKMRFHQLFSQDWPHPTFAVM 368
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 QY 366 OQNSNPALRQLPRLPILSILPLILQLTLW 397
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Db 369 AHQENPAVRPQWPVPSLFSCTLPILLLSLW 400
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RESULT 15
 AAW84186
 ID AAW84186 standard; protein; 400 AA.
 XX
 AC AAW84186;
 XX
 XX 25-MAR-1999 (first entry)
 XX
 XX Glial cell line-derived neurotrophic factor receptor gamma 2.
 DE
 DE Glial cell line-derived neurotrophic factor receptor gamma 2.
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 XX
 OS Homo sapiens.
 FH
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT /label= signal_peptide
 FT Protein 32..400
 FT /label= mature_protein
 FT Domain 32..382
 FT /note= "extracellular domain"
 FT Domain 383..400
 FT /note= "transmembrane domain"
 XX
 XX WO9853069-A2.
 XX
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WO-US010328.
 PF
 XX 20-MAY-1997; 97US-0047092P.
 XX 27-JUN-1997; 97US-00884638.
 PR

```
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Hsu T, Young P, Gentz RL, Ruben SM;
XX
XX WPI; 1999-070150/06.
XX N-PSDB; AAV99334.
XX
XX New isolated glial cell derived neurotrophic factor receptors - used to
XX develop products for treating e.g. neurodegenerative disorders,
XX PT schizophrenia, hypertension, tumours, renal disorders, kidney failure or
XX PT gut dysfunction.
XX
XX Claim 53; Fig 7A-D; 156pp; English.
XX
XX The present sequence represents a glial cell line-derived neurotrophic
XX factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
XX with GDNFR-alpha, which is capable of complexing with glial cell line-
XX derived neurotrophic factor (GDNF) and mediating cell response to GDNF.
XX The GDNFR polypeptides and agonists can be used for treating disorders
XX associated with decreased activity of the respective polypeptides. They
XX can be used for treating neurodegenerative diseases such as amyotrophic
XX lateral sclerosis, Parkinson's disease, schizophrenia, insomnia, tardive
XX dyskinesia, hypertension, pituitary adenomas, hyperprolactinemia, thyroid
XX tumour, renal disorders, kidney failure, gut dysfunction, or for
XX regeneration of cardiomyocytes, epithelium or hepatocytes. Antagonists of
XX the polypeptides can be used for treating disorders associated with
XX increased activity of the respective polypeptides. The products can also
XX be used for detection, diagnosis and drug screening
XX
XX Sequence 400 AA;
XX
Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 4.9e-151;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
QY 7 PRPP-LMILLVLSLPLGAGNSLATENRFVNSCTQARKKEANPACAAOHLGSGCT 65
Db 9 PLPPVLMILLPLPPSLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAYHLLDST 68
QY 66 SSLSRPLPLESAMSADCLAEOLRNSLLIDCECHRMKHQATCLDIYVTVHPARSLGD 125
Db 69 SSISTPLPSEPSVFADECLAEOQLRNSLLIGCMCHRMKNQVACLDIYVTVHRAESLGN 128
QY 126 YELDVSPYEDVTVTSKPKWMLSKLMLKPDSDLCCLKFAMLCCLHDKCDRLRKAYGEACSG 185
Db 129 YELDVSPYEDVTVTSKPKWMLSKLMLKPDSDLCCLKFAMLCCLHDKCDRLRKAYGEACSG 188
QY 186 IRCQRHLCALQLRSFFFEKAAESHAQGLLLCPCAPEDAGCGERRNTIAPSCALPSVTPNC 245
Db 189 PHCQRHVCLQLLTFPEKAAEPHAQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNC 248
QY 246 LDLSRFRADPLCRSLRMDFTQCHPMDDILGTCTATEQSRCLRAYLGLIGTAMTPNFISKV 305
Db 249 LELRLCFSDPLCRSLRVDFQTHCHPMDDILGTCTATEQSRCLRAYLGLIGTAMTPNFVSNV 308
QY 306 NTTVALSCTCRGNSNLQDECEQLERSFSQNPCLVEATAAKMRHQLFSODWADSTFVV 365
Db 309 NTSVALSCTCRGNSNLQEECEMLEGFFSHNPCLTEATAAKRHFHSQLFSDWPHPTFAVM 368
QY 366 QQQNSNPALRQLPLPILFSLPILPILLOTLM 397
Db 369 AHQNPENAVRPQWPVPSLFCSTPLILLLSLM 400
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